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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pland is derived by analysis of the total score distribution. printed,

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۵	ш	Result No.
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600 42 AI099199	675 64 AL119269	IJ
AI099199 ue40c07.y	AL119269 DKFZp761M	esult Query No. Score Match Length DB ID Description

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AL119269 675 bp mRNA EST 27-SEP-1999 DKFZP761M0513_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZP761M0513 5', mRNA sequence.
AL119269 1 GI:5925168 EST.
                     MIPS
Am Klopferspitz 18a D-82152 Martinsried, Gei
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Ana
Research Center (DKFZ); Email s.wiemann@dkfi
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Catarrhini; Hominidae; Homo
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    the cDNA sequencing
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                     r Genome Analysis, German Cancer
wiemann@dkfz- heidelberg.de;
                                                                                                                                                                                                                                 Mewes, H.W.,
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R59283 Y997h01.r1
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AR308005 VC85b01.y
AR3086386 MD97c11.y
AR309244 LI-BT202-AW139646 UI-H-BI1-AW139646 UI-H-BI1-AW139646 UI-H-BI1-AW13966 Drosophil AL103986 Drosophil AL103986 Drosophil AL103986 Drosophil AM8907876 MD97c1.r
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AR47818 YJ56c04.r1
AR890787 MJ56h10.s
AR47818 YJ56c04.r1
AR890787 MJ56h10.s
AR47818 YJ56c04.r1
AR89071 J34A05.y
AR687472 NS16h10.s
AR49071 J34A05.y
AR687472 NS16h10.s
AR89071 J34A05.y
AR687472 NS16h10.s
AR89071 J34A05.y
AR68747 NS16h10.s
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AR68747 NS16h10.s
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AR30877 WJ51c07.x
AR1018543 OU30-10.x
AR13715 UI-R-C12-AR313715 UI-R-C13-AR313715 UI-R-C12-AR313715 UI-R-C12-AR313715 UI-R-C12-AR336846 ZR76h12.r
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AI099199 600 bp mRNA EST 20-AUG-1998 ue40c07.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1482828 5' similar to WP:T20G5.5 CE00479 CAMP DEPENDENT PROTEIN KINASE REGULATORY CHAIN + GUANINE NUCLEOTIDE RELEASING FACTORS ; mRNA sequence.
AI099199
AI099199.1 GI:3448724
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No sl sequence available.

This clone is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DkFZp761M0513"
/clone_lib="761 (synonym: h:
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="pH108"
/note="Vector: pSport1; Sit
a 172 c 158 g 166 t
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454 358 394 298 334

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

Homo sapiens
Eukaryota; Metazoa; Chc
Eutheria; Primates; Cat
1 (bases 1 to 675)
Ansorge, W., Benes, V., i

COMMENT

EST (Ansorge, Benes, of Unpublished (1999) On Jun 22, 1998 this secontact: Ansorge W

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Wiemann, S.

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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Apr 18, 1995 this sequence vers Contact: Marra M/Mouse EST Project
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On Apr 18, 1995 this sequence version
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house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be used to isolate the CDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); Ist strand cDNA (CACTGTGTG); Site_2: DraIII (CACCATGTG); Ist strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was
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92.3%;
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Pred. No. 3.2e-139;
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                                                                                                                                                                                                                                                                                  Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cance Research Center (DKFZ); Emmil s.wiemann@dkfz- heidelberg.de; sequenced by GBF within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
On Jun 22, 1998 this sequence version replaced
Contact: Bloecker H
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DKFZp761D0424_r1 761 (synonym: h
DKFZp761D0424 5', mRNA sequence.
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EST.
                                                                                                                                                                                                   This clone is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                       German Genome Project
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                                                                                                                                                                                                                                                    No s1 sequence available.
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                                                             /clone="DKF2p76iD0424"
/clone_lib="761 (synonym:
/tissue_type="amygdala"
/dev_stage="adult"
                                  /note="Vector:
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/db_xref="taxon:9606"
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Query Match Best Local Similarity Matches 405; Conserv

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Score 402.6; DB 64 Pred. No. 8.1e-104; 0; Mismatches 4;

DB 64;

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                                                                                                                                                                                             Email: est@watson.wustl.edu
Insert Size: 451
High quality sequence stops: 315 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 451 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R59283 446 bp mRNA EST 24-MAY-1995
y997h01.r1 Soares infant brain 1NIB Homo sapiens cDNA clone
IMAGE:41798 5' similar to SP:T20G5.5 CE00479 CAMP DEPENDENT PROTEIN
KINASE REGULATORY CHAIN + GUANINE NUCLEOTIDE RELEASING FACTORS ;,
                                                                                                                                                                                                                                                                                                                                                                                 The WashU-Merck EST
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Location/Qualifiers
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314 286 1800
314 286 1810
                                                     /db_xref="taxon:9606"
/clone="IMAGE:41798"
                 /clone_lib="Soares infant brain
/sex="female"
                                                                                       /organism="Homo sapiens"
/db_xref="GDB:414339"
/dev_stage="73 days
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gtgattgacaaccagagaactttatcacagatgtcacacagattagagcctcgtcgacca 2953
                                                         cycatyattycaaatacyyccayaacaytyayatactacayyayccaacccttcaatcct 2833
                                                                                                                             acatttactcatgaggggaacaagacgttcattgacaatctagtaaactttgaaaaaaatg 2773
                                                                                        CGCATGATTGCAAATACGGCCAGAACAGTGAGATACTACAGGAGCCAACCCTTCAATCCT
                                                                                                                     ACATTTACTCATGAGGGGAACAAGACGTTCATTGACAATCTAGTAAACTTTGAAAAAATG 179
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98.6%;
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Pred. No. 2.1e-99;
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RESULT
AU079207
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KEYWORDS
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                                                                                                                    JOURNAL
                                                                                                                                                   TITLE
                                                                                                                                                                                  AUTHORS
            Eutheria; Rodentia; Sciurognathi; Muridae; N
1 (bases 1 to 541)
1 (bases 1 to 541)
Hashimoto, K., Kusuda, J., Toyoda, A., Tanuma, I
Suzuki, Y., Sasaki, M. and Sugano, S.
Isolation of full-length cDNA clones from a
library made by oligo-capping method
Unpublished (1999)
On Jun 22, 1998 this sequence version replac
Contact: Ratsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162
Email: khashi@nih, 90, jp
                                                                                                                                                                                                                                                                                                                 AU079207
AU079207
5', mRNA
AU079207
                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Ver
Eutheria; Rodenția; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                   house mouse
                                                                                                                                                                                                                                                                                                  AU079207.1
 http://www.nih.go
                                                                                                                                                                                                                                                                                                                                 sequence.
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Sugano mouse
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jp/yoken/genbank,
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                                                                                              replaced
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                                162-8640,
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                                                                                                                                                                                                               Murinae;
                                                                                                                                                mouse
                                                                                                                                                                                                                                                                                                                                              cDNA clone MNCb-3986
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AUTHORS
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VERSION
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AW047433/c
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                              aaactgccaagcaagttcaagaagttctatgcggagtttgaaagtttaatggacccttca
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                                                                                                                                                                                                                                                                                                                                                            ATGCCCTTGCTTATTAAAGATATGACATTTACTCATGAGGGGAACAAGACGTTCATTGAC
                                                                                                                                                 AWU47433 411 bp mRNA EST UI-M-BH1-all-c-07-0-UI.Sl NIH_BMAP_M_S2 MUS UI-M-BH1-all-c-07-0-UI 3', mRNA sequence.
1 (bases 1 to 411)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two appr
                                                                                                                       EST
                                                 Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                     Mus musculus
                                                                                                       house mouse
                                                                                                                                     AW047433.1 GI:5907962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTTTTTTTT] double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG] , digested and cloned into dstinct DraIII sites of the pME18S-FL3.

XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer for sequencing: 5' end primer [CTTCTGCCTCTAAAACCTGCG]"
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/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="MNCb-3986"
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                                                 Chordata; Craniata; Ver
Sciurognathi; Muridae;
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Pred. No. 1.4e-86;
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ae; Murinae;
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                        2194 aggcccaactgttggaacagtgggaacttttgaactgatgagctccaaagatttagcata
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                                                                                                                                                                                                                                                                                                                                         acgcctgtttgcttgcccgcgagagcaattcgattcactgactcccttaccagaacagga 2193
                                                                                                                                                                    AGAAAAGGTGGTGCTGAAATCTAATGATGTTTCAGTATTTACGACGCTCACCATTAATGG
                                                                                                                                                                                           agaaaaggtggtgctcaaacctaatgatgtttccagtatttacgacgctcaccattaatgg 2133
                                                                                                                                                                                                                                                       AGTAGCTGACAAACTGGGCTCAGGGGGAAGGCCTGATAATCGTCAAGATGAACTCTGGAGG
ACGCCTGTTTGCCCTGACAGAGAGCAATTCGACTCACTGACTCCCTTGCCGGAACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, the record will be updated accordingly when that means is determined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on Jun 5, 1998 this sequence versio
Contact: Chin, H
National Institute of Mental Health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301 443 1706 Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13 Forward POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20892-9643,
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TAG_LIB=NIH_BMAP_M_S2
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/clone_lib="NIH_BMAP_M-82"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAG_TISSUE=corpus-striatum
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Pred. No. 6.6e-82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Sep 12, 1996 this sequence version replaced Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project WashIngton University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 361)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vc85b01.rl Ko mouse embryo 11 5dpc Mus musculus cDNA clone IMAGE:789769 5' similar to WP:T20G5.5 CE00479 CAMP DEPENDENT PROTEIN KINASE REGULATORY CHAIN + GUANINE NUCLEOTIDE RELEASING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
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314 286 1810
                                            quality sequence stop: 327.
             b
                              constructed
                                                                                                                                                                                                                                     /tissue_type="embryo"
/dev_stage="11.5dpc"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                           /clone_lib="Ko mouse embryo 11 5dpc"
                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:789769"
                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                               /sex="pooled"
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                   by Dr. Minoru S. H. Ko and Dr. Xiaohong
           78
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                                                                                                                                                                                                                                Tel:
                                                                                                                                                                                                                                                                         Contact: Wilson RK
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                   /sex="male"
                                                                                                  Location/Qualifiers
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2595 tctatgcggagtttgaaagtttaatggacccttcaagggaaccacagggcctacagggctga 2654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atgcagctcaagctaataagaaccatcaggatgtccggagttatgtacggcaattaaatg
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Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2285771.
                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence.stop: 269.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
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1 (bases 1 to 317)
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/tissue_type="schizophrenic brain S-11 frontal lobe"
/dev_stage="34 years old"
                                                                                        /clone="IMAGE:1683900"
/clone_lib="Stratagene schizo
                                                                                                                                                  /db_xref="taxon:9606"
                                                                                                                                                                             /organism="Homo sapiens"
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Pred. No. 6.6e-79;
0; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Box 8501, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL120018 343 bp mRNA
DKFZp761H222_r1 761 (synonym: b
DKFZp761H222 5', mRNA sequence.
AL120018
                                                                                                                            Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5', sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
                                                                                                                                                                                                                                   Unpublished (1999)
On Jun 22, 1998 this s
Contact: Ottenwaelder
This clone is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 343)
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                                                                      No s1 sequence available.
                                                                                       the German Genome Project.
                                                                                                           sequenced by MediGenomix within
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                                                                                                                                                                                                                                      1998 this sequence version replaced gi:3247395 ttenwaelder B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:5925917
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(synonym: hamy2) Homo
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                                                                                                             the cDNA
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AUTHORS
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                                   FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
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Best Local S
Matches 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2783 gcaaatacggccagaacagtgagatactacaggagccaacccttcaatcctgatgcagct 2842
                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caagctaataagaaccatcaggatgtccggagttatgtacggcaattaaatgtgattgac 2902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI205130 268 bp mRNA an04h10.x1 Stratagene schizo brain IMAGE:1684675 3', mRNA sequence.
                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyT not found
Seq.primer: -40UP from Gibco
                                                                                                                                                                                                                                                WashU-NCI human EST Project
Unpublished (1997)
On Jan 19, 1998 this sequence version
                                                                                                                                                                                                                                                                                                     Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                           Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                     Contact: Wilson RK
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314 286 1810
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                                                  quality sequence stop: 240.
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/clone_lib="761 (synonym: hamy2)"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pSport1; 78 c 62 g 8
                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
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/organism="Homo sapiens"
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Pred. No. 4.7e-69;
0; Mismatches 4
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81 t
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ggacgcctgtttgcttgcccgcgagagc 2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAGAAAAGGTGGTGCTCAAACCTAATGATGTTTCAGTATTTACGACGCTCACCATTAAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGACGCCTGTTTGCTTGCCCGCGAGAGC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggagaaaaggtggtgctcaaacctaatgatgtttcagtatttacgacgctcaccattaat 2131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGTTGCCGACAAGCTGGGCTCCGGGGAGGGCCTGATCATAGTCAAGATGAGTTCCGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gcagttgccgacaagctgggctccggggagggcctgatcatagtcaagatgagttccgga 2071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI842094 450 bp mRNA EST 14-JUL-1999 UI-M-AN1-afg-e-01-0-UI.S1 NIH_BMAP_MBG_N Mus musculus cDNA clone UI-M-AN1-afg-e-01-0-UI 3', mRNA sequence.
                                                                                                                                                                                                        On Dec 20, 1995 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 450)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                    National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                                                                                                                                                                                         97044477
                                                                                                                                                                                                                                                            Genome Res. 6 (9),
                                                                                                                                                                                                                                                                                            discovery
                                                                                                                                                                                                                                                                                                             Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI842094.1 GI:5476307
                        Email: mEST@mail.nih.gov
                                                                                                       20892-9643, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse.
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sequence contained an oligo-dT track that was
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301 443 9890
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/dev_stage="34 years old"
/dev_stage="34 years old"
/lab_host="SOLR (kanamycin resistant)"
/note="vector: Bluescript SK-; Site_1: EcoR; Library
/note="vector: Bluescript Sk-; Shizophrenic suicide.
Sol caucasian, 50% Aleutian. Schizophrenic suicide.
Random primed into EcoRI site of ZAP II vector. Mass
excised. Custom library. Avg insert length 1.4kb.
Material obtained by Johnston N., Torrey, E.F., Yolken R.,
and the Stanley Neuropathology Consortium - Analysis of
RNAs from the Brains of Individuals with Psychiatric
Diseases (Unpublished) Stanley Neurovirology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."
63 a 68 c 76 g 61 t
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/clone_lib="Stratagene schizo brain S11"
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100.0%; Pred. No. 1.7e-65;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                            791-806 (1996)
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                                                                                                                                                                                                        gi:1133363
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FEATURES
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accaggatgctgtgaccatctgtaccctgggaattgggacggcctttggagagtccattc 274
                                                                                                                                                                            CCAACTGGTATGCTGTCCTGGCTGGGTCTTTGGATGTTAAAGTGTCTGAGACCAGCAGTC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized basal ganglia library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. Seq primer: M13 Forward
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TAG_SEG_TGTAC,

The library was constructed as describe

Tag_Seg_TGTAC,

Tag_Seg_TGT
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                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_MBG_N library is a normalized library constructed from mouse basal ganglia. The tag is a string of 5 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="UI-M-AN1-afg-e-01-0-UI"
/clone_lib="NHLBMAP_MBG_N"
/dev_stage="27-32 days"
/lab_host="DH10B_(Life_Technologies)"
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/db_xref="taxon:10090"
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93.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 263.2; DB 6
Pred. No. 4.9e-64;
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                                                                                                                                                                   tggctcctccttatggtattatggaaacgggctctaacaatgacaggattcctgacaagg
                                                                                                               AGAA 147
                                                                                                                                                          TGGCTCCTCCCTATGGTGTTATGGAAACGGGCTCTAACAATGACAGGATTCCTGACAAGG
                                                                                                                                                                                                                                                                                           ACCAGGATGCGGTGACCATCTGCACTCTGGGAATTGGGACAGCCTTTGGAGAGTCCATTC 331
mRNA sequence.
AI608196
AI608196.1 GI:4617363
                                vc85b01.yl Ko mouse embryo 11 5dpc Mus musculus cDNA clone IMAGE:789769 5' similar to TR:Q92565 Q92565 MYELOBLAST KIAA0277. ;,
                                                        AI608196
                                                      277 bp
                                                        mRNA
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                                                                        cagtagctaagctggaacctcctctcatccccttcatgcctttgctcattaaagatatga 2714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
On Jun 22, 1998 this sequence version replaced gi:3247167.
Contact: Marra M.Washu-NCI Mouse EST Project 1999
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra,M., Hillier,I., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R. Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 277)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ;
IMAGE Consortium (info@image.llnl.gov) for further ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
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                                                                                                                                                                                                                                                                                                                                   83
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: embryo; Vector: pSPORT1; Site_1: Sall; Site_2: Not1; Total RNAs were extracted from 11.5 dpc embryos (excluding placenta and yolk sac). The double-stranded CDNA was synthesized with an oligo (dT)-1
                                                                                                                                                                                                                                                                                                                                                                   constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="11.5dpc"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:789769"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="
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                                                                                                                                                                                                                                                        Score 239.8;
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                                                                                                                                                                                                                                                                                                                             59 g
                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                         .8; DB 48;
1.9e-57;
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Matches 302; Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Jun 15, 1998 this sequence version replaced gi:3225813. Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Watterfer, B., Roth, S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI:332812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
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314 286 1810
                                                                                                             /clone_lib="Stratagene mouse
/sex="female"
                                                                                                                                                                                                                                                                                                                                       /strain="C57BL/6 x CBA"
/db_xref="taxon:10090"
/clone="IMAGE:552020"
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                   7.3%;
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Score 220.4; DB 4
Pred. No. 7.8e-52;
0; Mismatches 137
                                       DB 45;
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                                       Length
                                        441;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAAAATCCCTGGGAAGTTTAAGAAGCTTTTCTCTGAACTTGAGAGTTTAACGGATCCTT
                                                                                                                                                                                                                    Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=IL&t2=IL-BT202-
                                                                                                                                                                                                                                                                                                                                      On Jun 5, 1998 this sequence version replaced Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 540)
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Seg primer: puc 18 forward.
Location/Qualifiers
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The FAPESP/LICR Human Cancer Genome Project
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IL-BT202-250399-011 1
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+55-11-2707001
   /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue
                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                    /dev_stage="Adult"
                                                                                                  /sex="female"
                                                                                                                 /clone_lib="BT202"
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             National Cancer Institute, Cancer Genomer Tumor Gene Index
Unpublished (1997)
On Jul 7, 1999 this sequence version recontact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausberg@nh.gov
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UI-H-BII-adr-c-04-0-UI.s1 NCI_CGAP_Sub3
IMAGE:2717575 3', mRNA sequence.
AW139646
                                                                                                                                                                                                                                                                                                                                                                                    533
Email: Robert_Strausberg@nih.gov
Oligo-dT track not found, Not I site shown
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 444)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGA
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Project (CGAP),

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Pred. No. 2.6e-50;
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CTGGACAACGCCGCTGTCAGCCGCCTTCGACTCACCTGGGAGAAGCTGCCAGGGAAATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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TAG_SEQ=GACAGC"
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/db_xref="taxon:9606"
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                                                                               gatatgacatttactcatgaggggaacaagacgttcattgacaatctagtaaactttgaa 2767
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Search completed: April 22, Job time: 9891 sec 2000, 11:27:55

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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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45: gb_htg7:*
46: em_htg1:*
47: em_htg2:*
48: em_htg3:*
49: em_hum5:*
50: gb_pl3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C 41 C 42 43 44 45	. C 354 354 398		14 15 15 16 17 18 17 18 21 21 22 23 24	0 0 5 4 4 3 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
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ALIGNMENTS

VERSION	ACCESSION		DEFINITION	LOCUS	HSU78516	RESULT 1
U78516.1 GI:4115908	U78516	(CAMP-GEFII) mRNA, complete cds.	Homo sapiens cAMP-regulated guanine nucleotide exchange factor II	HSU78516 4278 bp mrna PRI 08-Jan-1999		

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A family of cAMP-binding proteins that directly activate Science 282 (5397), 2275-2279 (1998)
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EKFHPNLLHQICLCGYYENLEKGITLFRQGDIGTNWYAVLAGSLDVKVSETSSHQDAV
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8	5 GGGAGGCCTGATCATAGTCAAGATGAGTTCCGGAGGAGAAAAGGTGGTGCTCAAACCTA	2	рь
2096	7 gggagggcctgatcatagtcaagatgagttccggaggagaaaaggtggtgctcaaaccta	203	Qy
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1916	7 ttcttttgcaacagttcaatacgggcgatgagagcccagaagcgccagcctatccgcg	5	οy
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1736	7 ccatgtatggagacctcctgcaagaggatgtatctatggccttcctggaggagtttt	167	Qy
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1744	5 CAGATTCTGTTTTAAATGACTTTATTATGATGCACTGTGTTTTTATGCCAAATACCCAGC	œ	рь
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1376 1564	7 gacttaaagaacatgaccaagatgtcttggtgctggagaaggtcccagcagggaacagag :	131 150	Оу

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Jolla, CA 92037,
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ACCESSION
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KEYWORDS
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JOURNAL
MEDLINE
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AUTHORS
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Institute of Technology, 77 Massachus
Cambridge, MA 02135, USA
On Jan 8, 1999 this sequence version
Location/Qualifiers
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A family of cAMP-binding proteins that directly activate rapl Science 282 (5397), 2275-2279 (1998)
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Springett,G.M., Kawasaki,H.,
Direct Submission
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                                                                             /translation="RVIRIVLQWAAMYGDLLQEDDVAMAFLEEFYVSVSDDARMMVAF
KEQLAELEKTYVGJISEDAKAPQKKHVYLLQQENTGDERAQKRQFIRGSDEVLEKVYGI
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AHCKEVALISPEGIVWGLSWVAESRLALTWEKLPSKFKKFYAEFESLMDFSRNHKAY
RLTAAKLEPPLIFMEYLIKDMTFHEGNKTFTDULLVHEEKSKBMIANTARTVRYYRSQ
PFNPDAAQANKNHQDVRSYVRQLNVIDNQRTLSQMSHRLEPRRP"

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factor II"
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/db_xref="GI:4115911"
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/note="similar to
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A family of cAMP-binding proteins that directly Science 282 (5397), 2275-2279 (1998)
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KMRMMARAARMLHHCRSHNPVPLSPLRSRVSHLHEDSQVARISTCSEQSLSTRSPAST
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/codon_start=1
/product="cAMP-regulated guanine nucleotide factor I"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     de Rooij,J., Zwartkruis,F.J., Verheijen,M.H., Cool,R.H., Nijman,S.M., Wittinghofer,A. and Bos,J.L.

Epac is a Rapl guanine-nucleotide-exchange factor direct activated by cyclic AMP
Nature 396 (6710), 474-477 (1998)
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1 (bases 1 to 2646)
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              APRAAT I I LREDNCHFLEVDKODFNR I I KDVEAKTMRLEEHGKVVLVLERASGGAGPS
RP PTFGRNRYTYNGGTPEK I LELLLEAMGEDSSAHDETETFLSDFLITHKVEMPSAQL
CAALLHHFHVEPAGGSEQERSTY VCNKRQQI I LELVSQWFALYGSMLHTDPVATSFLQK
LSDLVGRDTRLSNLLERDGWPERRCHRLENGGGNASFOMKARNLEVYLENDOEPLFGK
SCAIQVGDKVPYDICRPDHSVLTLQLPVTASVREVMAALAQEDGWTKGQVLVKVNSAG
SCAIQVGDKVPYDICRPDHSVLTLQLPVTASVREVMAALAQEDGWTKGQVLVKVNSAG
DAIGLQFDARGVATSLGLNERLEVVNNPQEAHELI PHEPOLGFTVGSABGLDLDVSAKDL
AGQLTDHDWSLENSIHQVELHYVLGFQHLRDVTTANLERFMRRFNELQFMVATELCL
CPVPGPRAQLLRKFIKLAAHLKEQKNLNSFFAVMFGLSNSAISRLAHTWERLLHKVRK
LYSALERLLDESWNHRVYRLALAKKLSPPVIFFMPLLKDMTFIHEGNHTLVENLINFE
                                                                                                                                                                                                                                                                                                 /translation="MVLRRMHRPRSCSYQLLLEHQRPSCIQGLRWTPLINSEESLDFS ESLEQASTERVLRAGRQLHRHLLATCPHLITDRKYHLRLYRQCGGRELYUGILAHGL GVHSRSQVUGICQVLLDEGALCHVKHDWAFQDRDAQFYRFGEBPEPVGTHEMEEELA EAVALLSQRGPDALLTVALRKPPGQRTDEELDLIFEELLHIKAVAHLSNSVKRELAAV
{\tt KMRMMARAARMLHHCRSHNPVPLSPLRSRVSHLHEDSQVARISTCSEQSLSTRSPAST}
                                                                                                                                                                                                                                                                     LLFEPHSKAGTVLFSQGDKGTSWYIIWKGSVNVVTHGKGLVTTLHEGDDFGQLALVND
                                                                                                                                                                                                                                                                                                                                                                                                             /product="Rapl guanine-nucleotide exchange
/protein_id="AAC83381.1"
/db_xref="GI:3978531"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="contains cAMP binding domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="muscle"
1. .2646
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                 tcttacgagaagataactgccatttcttaagagtagacaaggaggatttcaaccggatcc 1289
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                   -GTATACAGTGATGTCTGGCACCCCAGAGAAGATCCTAGAGCTTCTGTTGGAGGCCATGG
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A family of cAMP-binding proteins that directly activate Rapl Science 282 (5397), 2275-2279 (1998)
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KOLAGQLTEHWNLFRRIHQVELTHYVLGPQHRBUTTGALGERFMRRFRBLQYWVATE
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/note="GEF domain shows highest similarity family; contains cAMP binding domain"
/codon_start=1
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/db_xref="GI:4079657"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-AUG-1996) to the DDBJ/EMBL/GenBank databases. Nomura. Kazusa DNA Research Institute, Gene Structure 1; 153
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56. .1
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56. .1798
/gene="KIAA0277"
/note="Similar to a C.elegans
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/db_xref="taxon:9606"
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gccagtggccacttcggtgaaggaagtcatcagtgcagttgccgacaagctgggct---c
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LSQTWEKIPGKFKKLFSELESLTDPSLNHKAYRDAFKKMKPPKIPFMPLLLKDVTFIH
EGNKTFLDNLVNFEKLHMIADTVRTLRHCRTNQFGDLSPKEHQELKSYVNHLYVIDSQ
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EDDEWSSRSQSSTEDDSVDSLLSDRYVVVSGTPEKILEHLLNDLHLEEVQDKETETLL
DDFLLTYTVFMTTDDLCQALLRHYSAKKYQGKEENSDVPRRKRKVLHLVSQWIALYKD
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/db_xref="GI:1665819"
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 59255)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-22F10
Unpublished
                                                                                                                               AC016789 59255 bp DNA HTG 05-DEC-1 HOMO SAPIENS Clone RP11-22F10, LOW-PASS SEQUENCE SAMPLING. AC016789 1 GI:6538791 HTG; HTGS_PHASE0.
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Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrin, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassilev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                    Submitted (05-DEC-1999) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren, B., Linton, L.,
Center project name: L4108
Center clone name: 22_F_10
                                                                              Contact: sequence_submissions@genome.wi.mit.
                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                  Center code: WIBR
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                                                                                                                                                                                                                                                              Research
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sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will NOTE: This record contains 76 individual preserved. 755 1539: 754: contig of 754 bp in length gap of unknown length L539: contig of 785 bp in length

3047: 3841: 4639:

> contig gap of

unknown of 745 bp in unknown length

length

length length

contig gap of contig

gap of contig

gap of contig gap of contig

unknown lengt of 755 bp in unknown length of 798 bp in l unknown length of 794 bp in length of 763 bp in

length

length

length length length

unknown length of 751 bp in length unknown lengt of 763 bp in

10033 9263 8485 7693 6909 6158 5395 4640 3842 3048 2285 1540

gap of contig gap of contig gap of contig

gap of contig gap of contig gap of

unknown le of 775 bp unknown le

length

of 785 bp in of 784 bp in length unknown length

length

unknown

length

9262:

unknown lengt of 778 bp in

length

length length

unknown length of 770 bp in l

7692:

gap of contig gap of contig gap of contig

unknown length of 792 bp in length unknown length of 784 bp in length

40444	39671	38895	38102	37312	36548	35764	34974	34185	33421	32637	31881	31101	30300	29508	28729	27955	27172	26380	25639	24875	24107	23303	22515	21755	20981	20210	19408	18623	17844	17071	16285	15511	14735	13940	13154	12377
41210:		39670:	38894:	38101;	37311:	36547:	35763:	34973:	34184:	33420:	32636:	31880:	31100:	30299:	29507:	28728:	27954:	27171:	26379:	25638:	24874:	24106:	23302:	22514:	21754:	20980:	20209:	19407:	18622;	17843:	17070:	16284:	15510:	14734:	13939:	13153:
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n length	n length	in length	n length	n length	n length	n length	n length	n length	n length	n length	n length	p in length	p in length	p in length	p in length	ingth in length	p in length	p in length	length p in length	p in length	p in length	p in length	p in length	length p in length	p in length	length p in length	length p in length	length p in length	p in length	p in length	p in length	p in length	length p in length	length p in length	in length	n length

RESULT 9 AC014497 AC014497 AC014497 AC014497 AC014497 AC014497 AC014497 DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered pieces. ACCESSION VERSION VERSION CO14497 AC014497 AC014497 AC014497 GENERAL ACO14497 FIGS_PHASE2. SOURCE SOURCE Fruit fly. ORGANISM Drosophila melanogaster	Qy 3009 a 3009 Db 46135 A 46135	QY 2949 gaccatagacatttcaaatgcccaaagcaacagtttgtctccagtccacaattttcaaaa 3008 	Qy 2889 taaatgtgattgacaaccagagaactttatcacagatgtcacacagattagagcctcgtc 2948 	Qy 2829 atcctgatgcagctcaagctaataagaaccatcaggatgtccggagttatgtacggcaat 2888	Query Match 5.8%; Score 176.2; DB 44; Length 59255; Best Local Similarity 98.3%; Pred. No. 1.3e-38; Matches 178; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	56878: contig of 788 bp in gap of unknown lengt	* 54499 55290; CONLIG OF 798 DP IN LENGTH * 55297 56090; Contig of 794 bp in length * 55297 56090; Contig of 794 bp in length	53729 54498; contig of 770 bp in 53729 gap of unknown lengt	gap of un 52937 53728: contig of un	513// 52156: contig gap of 52157 52936: contig	51376: contig of 773 bp in gap of unknown lengt	gap of unknown 49811 50603: contig of 793 b	gap of unknown lengt 49017 49810: contig of 794 bp in	of 770 h unknown	* 46707 47484: contig of 778 bp in length * 46707 47484: contig of 778 bp in length	unknown of 783 k	gap of unknown lengt 45139 45923; contig of 785 bp in	gap of unknown lengt 44335 45138: contig of 804 bp in	43549 44334: contig	contig of 784 bp in gap of unknown lengt	gap of unknow 41988: contig of 778 gap of unknow

COMMENT

TITLE

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AUTHORS
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AC007549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster chromosome 2 clone BACR04F03 (D622) RI 04.F.3 map 42D-42E strain y; cn bw sp, *** SEQUENCING IN PROGRESS. 79 inordarad vicana
              Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, Butenboff, C., Champe, M., Chavez, C., Chew, M., Clestolka, L., Doyle, C.M., Farfan, D.E., Galle, R., Goorge, R.A., Harris, N. L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Meille, J.M., Park, S., Meille, J.M., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Meille, J.M., Meille, J.M., Park, S., Meille, J.M., Park, S., Meille, J.M., Meille, J.M., Park, S., Meille, J.M., Park, S., Meille, J.M., Park, S., Meille, J.M., Meille, J.M., Park, S., Meille, Park
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 111455)
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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
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Pfeiffer,B., Poon,L., Sequeira,A.,
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e-mail to fly@celera.com
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                                                                                                Kearney, L.,
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For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 79 contigs. The true order of the pleces is not known and their order in this sequence record is
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* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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1539: contig of 716 bp in length
1519: gap of unknown length
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of unknown .

Alig of 1103 bp .

Alig of 10103 bp .

Tap of unknown length

Tig of 987 bp in length

Minown length

Tig of 980 bp in length
g of 784 bp in length
g of 1167 bp in length
g of 1167 bp in length
if unknown length
g of 2150 bp in length
f unknown length
if unknown length
g of 1547 bp in length
g of 1692 bp in length
g of 281 bp in length
f unknown length
g of 2981 bp in length
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g of 1961 bp in length
g of 197 bp in length
if unknown length
g of 1693 bp in length
g of 197 bp in length
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Drosophila melanogaster chromosome
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38203 36860: 36940:

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40663: 41968: 42048: 43263:

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43343:

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29882: 31625: 31705:

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45899: 46912: 46992: 48172: 48252: 49636: 49716: 50819: 50899:

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64465: 64545: 66586: 66586: 67862: 67942: 69635: 69635: 70912: 70992: 73167: 73167:

59385: 60932: 61012: 62104:

62184

54964: 55044: 55828: 55908: 57075: 57155: 59305:

51886: 51966: 53335: 53415:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Celniker, S.E., Agbayanı, A., Chew, M., Clesacan, Butenhoff, C., Champe, M., Chavez, C., Chew, M., Clesacan, Butenhoff, C., Champe, M., Chavez, C., Chew, M., Clesacan, C., Harris, N.L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Hoskins, R.A., Houston, K., Li, P., Lomotan, M.A., Mazda, P., Kim.E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Kim.E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Kim.E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Kim.E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Kim.E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Kim.E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Kim.E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Kim.E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Kim.E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Kim.E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Kim.E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Kim.E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Kim.E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Kim.E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Kim.E., Lee, B., Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-MAY-1999) Drosophila Genome Center, Lawrence Berk Laboratory, MS 64-121, Berkeley, CA 94720, USA On Aug 2, 1999 this sequence version replaced gi:4887256. For further information about this sequence, including its loca and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send en to bdgp@fruitfly.berkeley.edu. All contlys in this submission m the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E., Syirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim.B., Lee,B., Lewis,S., Li.P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,
Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L
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Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney
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Park,S.,

and

Kearney, L.,

Blazej, R.G.,

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                Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E.,
                                                                                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                    ACU08340 125681 bp DNA HTG 06-AUG-1999
Drosophila melanogaster chromosome 2 clone BACR07J20 (D918) RPCI-98
D7.J.20 map 42D-42E strain y; cn bw sp, *** SEQUENCING IN PROGRESS
    Svirskas, R.R., Wan, K.H.,
                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE1.
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a 41017 c 40764 g 52607 t 4241 others
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /map="42E-43A"
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    Weinburg, T.,
    Zhang, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-AUG-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Aug 4, 1999 this sequence version replaced gi:5670395. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All_contigs in this submission meet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L. Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearne,
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* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draw sequence. It currently

* consists of 92 contigs. The true order of the pieces

* is not known and their order in this sequence record in
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be preserved.
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75697: 75777: 79775: 79855: 83769: 83849: 87287: 87367: 94193: 94273: 94273: 98243: 98323:

	TITLE JOURNAL COMMENT	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS
Center: WhiteHead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu Center clone name: 14108 Center clone name: 2210 **NOTE: This record contains 76 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. **However, it should not be assumed that this clone **Will be sequenced to completion. In the event that the record is updated, the accession number will **Deserved.** 755 1539: contig of 754 bp in length 2285 3047: contig of 755 bp in length **South of the same length **South of the same length **South of the same length **Add 3841: contig of 753 bp in length **South of the same len	Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Marquis, N., McEwan, P., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M. Direct Submission Submitted (05-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html	to 59255) inton,L., Nusl , clone RP11-; to 59255) inton,L., Nusl Barna,N., Bec stle,A., Colar Arellano,K., 1
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AC005285 209071 bp DNA INV 15-JUL-1998 Drosophila melanogaster DNA sequence (PIs DS00121 (D128), DS054 (D270), and DS00108 (D120)), complete sequence. AC005285 AC004272 AC002537 AC002638 AC003139 AC003717 AC003718 AC003140 AC003141 AC003719 AC002639 AC003142 AC003720 AC003143 AC004568 AC004269 AC002586 AC002586 AC003143 AC004568 AC004569 AC002586 AC002586 AC003131 AC003709 AC002585.1 GI:3320127
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Library locations: 25-2, 137-57, 12-2.
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Svirskas, R.R., Harris, N.L., Agbayani, A., Arcalna, T.T.,
Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E.,
Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,
Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S.,
Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacibe, J.M., Park, S.,
Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R.,
Yee, A., Zhang, R., Zieran, L.L. and Kimmel, B.E.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-JUL-1998) Berkeley Drosophila Genome Project, 64-121, Lawrence Berkeley National Laboratory, One Cyclotror Review, CA 94720, US Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
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Drosophila melanogaster
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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a 45615 c 45383 g 58488 t
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/db_xref="taxon:7227"
/chromosome="2L"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagase,T., Ishikawa,K., Nakajima,D., Ohira,M., Seki,N., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O. Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro DNA Res. 4 (2), 141-150 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nomura, Kazusa DNA Research Institute, Gene Structure 1; 1532-3 Yana, Kisarazu, Chiba 292, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:+81-438-52-3930,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax:+81-438-52-3931)
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                                                             /translation="MKPLAIPANHGVMGQQEKHSLPADFTKLHLIDSLHPQVIHVSSS
HSGCSITSDSGSSSLSDIYQATESEAGDMDLSGLPETAADSEDDDEED1ERASSPLM
SRDIVRBCLEKDPIDETDD1EQLLEEMHQLEAFANNTMSVUREELCAVWPEAVVERAG
TIVLNDGEELDSWSYILNGSVEVTYPDGKAEILCMGNSFGVSPTMDKEYMKGVMRTKV
                                                                                                                                                                                                                                           /gene="KIAA0313"
63. .4562
                    DDCQFYCIAQQDYCRILNQVEKNMQKVEEEGEIVMVKEHRELDRTGTRKGHIVIKGTS
ERLTMHLVEEHSVVDPTFIEDFLLTYRTFLSSPMEVGKKLLEWFNDPSLRDKYTRVVL
                                                                                                                                                 /codon_start=1
/protein_id="BAA20772.1"
/db_xref="GI:2224567"
                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HG0186"
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(28-MAR-1997) to the DDBJ/EMBL/GenBank databases. Nobel (28-MAR-1997) to the DDBJ/EMBL/GenBank databases. Nobel (28-MAR-1997) to the DDBJ/EMBL/GenBank databases.
                                                                                                                                                                                                                                                                                                                             /sex="male"
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LWVNNHFNDFEGDPAMTRFLEEFENNLEREKMGGHLRLLNIACAAKAKRRLMTLTKPS
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VEQVIGLEKVNIKKSKANTVGGRIKKLKKILDKTAISILPQKPYNIDIGIGQSODDSIVGL
RQTKHITTALPVSGTLSSSNPDLLQSTATPDLPQVLRVFKADQQSRYIMI
SKDTTAAERVJLQAIREEAVTAPPDQYSLCEVSVTPEGYIKQRRLPDQVSLKELDRIQLS
GRYYLKNIMETETLCSDEDAQELLRESQISLLQLSTVEVATQLSMRNFELFRNIEPTE
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MDPALMFRTRKKKWRSLGSLSQGSTNATVLDVAQTGGHKKRVKSETSPVARRASKIL
SGLSQGLQVFAVSLYENSKKYPVKDLFPFGINSPQALKKIL
SLSEEGSLERHKKQAEDTISNASSQLSSPFSPOSPRKGYTLAPSGTVDRESDSGHS
EISSRSSIVENOSCHOPVSLEDERRQBHSVSIVETNLGMERERRTMIEPDQYSLGS
YAPMSEGRGLYATATVISSPSTEELSQDQGDRASLDAADSGRGSWTSCSSGSHDNIQT
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QSRASWASSTGYWGEDSEGDTGTIKRRGGKDVSIEAESSLTSVTTEETKPVPMPAHI
AVASSTTKGLLARKEGKYREPPTFPGYIGIPTDFFGHSHARKPDYNVALQRSR
MVARSSDTAGPSSVQQPHGHPTSSRPVNKPQWHKPNESDPRLAPYQSQGFSTEEDEDED
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              tttgaaaaaatgcgcatgattgcaaa
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-371-377-16
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US-08-026-138E-6
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US-08-617-697-6
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1026.159 Million cell updates/sec
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Patent No. 5225348
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US-08-232-463-14/c
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NS-08-4/4-03A-70 PCT-US92-06412-8 US-08-182-175A-32 US-08-182-175A-34 US-08-474-633A-29 US-08-474-633A-29 US-08-474-633A-31 PCT-US92-06412-34 US-08-182-175A-90 US-08-182-175A-90 US-08-182-175A-90 US-08-182-175A-90 US-08-182-175A-90 US-08-676-974-2 US-08-676-974-2 US-08-676-974-2 US-08-676-974-2 US-08-676-974-2 US-08-105-483-222 US-08-670-151-75	Sequence

ALIGNMENTS

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US-08-232-463-14 PTZgpt-F1s
                                                                                                                                                     APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMPLECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)83-4109
TELEPX: 899149
INFORMATION FOR SEQ ID NO: 14:
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GENERAL INFORMATION:
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                               STRANDEDNESS: s
TOPOLOGY: lines
IMMEDIATE SOURCE:
CLONE: pTZgpt-F
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APPLICANT: SCHEITLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: 2313-0299
ZIP: 22313-0299
COMPUTER READABLE FORM:
COMPUTEM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 1
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                             FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley a _____
STREET: 1800 Diagonal Road,
                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                        LENGTH:
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     APPLICATION UNMBER: US/08/318/83
FILING DATE: 19 October 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: FR92/04827
FILING DATE: 21-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie K.
REGISTRATION UNMBER: P-38,619
REGISTRATION UNMBER: ST92033
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                        APPLICANT: Schweigholiet, acception APPLICANT: Tocque, Bruno APPLICANT: Tocque, Bruno APPLICANT: Tocque, Bruno PEPTIDES HAVING A GDP EXCHANGE FACTOR TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODITITIE OF INVENTION: PREPARATION AND UTILIZATION

TITLE OF SEQUENCES: 12
                                                                                                                                                              OPERATING SYSTEM: System 7.1 SOFTWARE: WORD 5.1 (EPO Pate CURRENT APPLICATION DATA:
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc
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                                                                                                                                                                                                                                                   ZIP: 19426
                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                              STATE:
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; LOCATION:
US-08-318-831-1
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Best Local Similarity
Matches 247; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (610) 454-3808 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
   2261
                               2757
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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                                                                                  tcattaaagatatgacatttactcatgaggggaacaagacgttca---ttgacaatctag 2756
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TCAACTTCTCCAAGATGAGGATGATATCCCATATTATCCGA
                                                              ACCTCACCGACCTGGCCTTCATCGAGGAGGGGGACGCCCAATTACACGGAAGACGGCCTGG
                                                                                                                                                                                            AGCAGACTAAAGCTTTGATTGATAAGCTCCAAAAGCTTGTGTCATCTGAGGGCAGATTTA
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RESULT 3
US-08-870-518-7
; Sequence 7, Application US/08870518
; Patent No. 5925566
; GENERAL INFORMATION:

2140 2639

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2020

2080

APPLICANT:

Davis,

APPLICANT: Galcheva-Gargova, Zoya
TITLE OF INVENTION: NON-ACTIVATED RECEPTOR COMPLEX

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US-08-371-377-16
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Best Local Similarity
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                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Fisher,
APPLICANT: Shen, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fasse, Peter J.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/870,518
FILING DATE: 06-UUN-1997
PRIOR APPLICATION DATA:
APPLICATION UNBER: 60/019,219
FILING DATE: 06-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                             NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                         2638 cagggcctacaggctgacagtagctaagctggaacctcctctcatccccttcatgccttt 2697
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LENGTH: 5183 base pairs
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                     TITLE OF INVENTION: DEVELOPMENT OF DNA PROBES AND
TITLE OF INVENTION: IMMUNOLOGICAL REAGENTS SPECIFIC FOR CELL SURFACE-EXPRESSED
TITLE OF INVENTION: MOLECULES AND TRANSFORMATION-ASSOCIATED GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1970 AAGACTGGTGGAAATTCCACCCAAAGGTCGAAAAATTACTTTAAAGGTCATGGATGCC 2029
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TELEFAX: ci.,
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STRANDEDNESS: single
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 COUNTRY:
                                                                                                                                                                                                                                                                                                                                 GGACTTGA 2097
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United States of America
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for Windows Version
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Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Lewis, I
APPLICANT: Xu, Min
APPLICANT: Hinman,
                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                     NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
CITY: Falls Church
STATE: Virginia
                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: TOLATED DAA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1633 TTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGG 1692
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LENGTH: 2128 base pairs
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
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OPERATING SYSTEM:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                          COUNTRY:
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                                                                                                        U.S.A.
                                                                                                                                                                                                                                                                                                    Xu, Ming
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1.1;
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 Version #1.25
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ATTORNEY/AGENT INFORMATION:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 19-APPLICATION: 435

19-APR-1995

US/08/425,069

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RESULT 6
US-08-317-844B-1
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PAGES: 7120-7124
PATE: Sept.-1990
RELEVANT RESIDUES IN SEQ ID
US-08-425-069-1
                                                                                                                                                                                                                  Sequence 1, Application US/08317844B Patent No. 5989894
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Best Local Similarity
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                                                                                      APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THERE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5989894th Washington Street
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CE
HYPOTHETICAL: NO
ORIGINAL SOURCE:
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LENGTH: 2338 base pairs
                                                                         NUMBER OF SEQUENCES:
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OTHER INFORMATION: /pi
OTHER INFORMATION: dra
PUBLICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     906 ggatgatccttcgcaaaccacctggccagaggactgtggatgacctaga 954
                                                                                                                                                                                                                                                                                                                                                                                                  495 TGGACAAGGTGCAGGTGCAGCAGCAGCAGCCGGAGGTGCTGGACAAGGCGGATACGG
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LOCATION: 1...
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AUTHORS: Lewis, R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703) 205-80
(703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lewis, Randolph V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34.6; DI
Pred. No. 1.2;
0; Mismatches
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US-08-026-138E-17
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                                                           Sequence 17, Application Patent No. 5502166
                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
GENERAL INFORMATION:
APPLICANT: Masayoshi
TITLE OF INVENTION: N
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2338 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TRETEBUOUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 1..2154
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                            906 ggatgatccttcgcaaaccacctggccagaggactgtggatgacctaga 954
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                                                                                                                                                                                                                                         846 atgaggagctccaggacaccatgctgctgtcacagatgggccccgacgcccacatga 905
                                                                                                                                                                                                                                                                                435 TGCTGGACAAGGAGGATATGGAGGTCTTGGAAGCCAAGGTGCAGGACGAGGTGGATTAGG 494
                                                                                                                                                                                                                                                                                                786 ttctggatgatgagcacgaggatgcccctttgcctactgaggaggaggagaagaaggagtgtg 845
                                                                                                                                                        555 TGGTCTTGGTGGACAAGGTGCCGGACAAGGAGGCTATGGAGGACTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rolerry "'
                                                                                                                                                                                                                                                                                                                                                                                                                                    PAGES: 7120-7124
DATE: Sept.-1990
RELEVANT RESIDUES IN SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE: Structure of a protein superfiber: TITLE: drafline silk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 04
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                      TGGACAAGGTGCAGGCAGCAGCAGCAGCCGGAGGTGCTGGACAAGGCGGATACGG 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lewis, Randolph V.
                                                                                                                                                                                                                                                                                                                                              Conservative
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004-OCT-1994
N. 127
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                 NOVEL
                                MISHINA
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dragline silk protein"
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                 PROTEINS
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Pred. No. 1.2;
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                 AND GENES
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US-08-026-138E-6
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            Sequence 6, Application US/08026138E
Patent No. 5502166
GENERAL INFORMATION:
APPLICANT: MASSYOSHI MISHINA
TITLE OF INVENTION: NOVEL PROTEIL
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US
FILING DATE: 26 FEB-15
FRIOR APPLICATION DATA:
APPLICATION NUMBER: JF
FILING DATE: 26 FEB-15
APPLICATION NUMBER: JF
FILING DATE: 30-JUN-15
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                                                                                                                                                                                                 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION:
AUTHORS: MASSYOSHI MISHINA
TITLE: NOVEL PROTEINS AND GENES CODING THE
RELEVANT RESIDUES IN SEQ ID NO: 17: FROM 1
                                                                                                                                                                                                                                2106
                                                                                                                                                                                                                                                                 1132
                                                                                                                                                                                                                                                                                                  2046
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FILING DATE: 12-AUG-1992
APPLICATION NUMBER: JP 303878/1992
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                  2166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: F-TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 986-2340
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: mouse
TISSUE TYPE: bra
                                                                                                                                                                                                                                                                                                                                                                                / Match 1.1%;
Local Similarity 54.9%;
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TOPOLOGY: lir
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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                                                                                                                                                                                                                               ATTCATCTACGATGCAGCCGTGCTCAACTACATGGCTGGAAGAGACGAAGGCTGCAAGCT 2165
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NOVEL PROTEINS
19
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               AND GENES
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to 43
               CODING
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TISSUE TYPE: brain

PUBLICATION INFORMATION:
AUTHORS: MASAYOShi MISHINA

TITLE: NOVEL PROTEINS AND GENES CODING THE SAME

RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 1 to 444

US-08-026-138E-6
                                                                                                                                   US-08-038-682-3
                                                                                                                                                           RESULT
Sequence 3, Application US/08038682
Patent No. 5549997
GENERAL INFORMATION:
APPLICANT: BARENKAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 26-FEB-1992
APPLICATION NUMBER: JP 173155/1992
FILING DATE: 30-JUN-1992
APPLICATION NUMBER: JP 215017/1992
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: JP 303878/1992
APPLICATION: Hamburg C BELICON:
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4446 nucleic acids
                                                                                                                                                                                                                                                                                                     2184
                                                                                                                                                                                                                                                                                                                            1132 agtcatttacggcaagggtgtggtctgcaccctgcatgaaggagatgacttcggcaagtt 1191
                                                                                                                                                                                                                                                                                                                                                                                                       1072 gtttaaccagggggaagaaggtacctcctggtacattattctaaaaggatcagtgaatgt 1131
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                                                                                                                                                                                                                    2244 GG
                                                                                                                                                                                                                                                          1192 ag 1193
                                                                                                                                                                                                                                                                                                                                                                                 2124 GTTCAACCAAAGGGGTGTAGATGATGCCTTGCTCCCCTGAAAACAGGGAAACTTGATGC 2183
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: (FILING DATE: 26-FEB-1 PRIOR APPLICATION DATA: APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 22
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Niigata-ken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 5214, Nis
CITY: Niigata-shi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                   ATTCATCTACGATGCAGCCGTGCTCAACTACATGGCTGGAAGAGACGAAGGCTGCAAGCT 2243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.18;
Similarity 54.98;
                                                                                                                                                                                                                      2245
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Word Perfect 5.1
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212) 953-7733
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CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: TITLE OF INVENTION:

8 FQ

NON-TYPEABLE HAEMOPHILUS

2001 Jefferson

Shoemaker and Mattare, 01 Jefferson Davis Hwy.,

Ltd , 1203 Crystal Plaza

PC-DOS/MS-DOS

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; MOLECULE TYPE:
US-08-038-682-3
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TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4937 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                          Sequence 3, Application US/08302832 Patent No. 5603938 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2469 CAACATGTCATTCAAATCTCAAAGAAGGAGCGAAAGTTAATTTCAAATTTAAAACCAAACGA 2528
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                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                        APPLICANT: Barenkan TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                      2529 GAACATGAACACAAGCAAACCTTTACCAATTCGGTTTTTAGCC 2571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/01
FILING DATE: 16-MAR-1993
CLASSIFICATION: 424
                                                                         COUNTRY: U.S.A.
                                                                                             CITY: Arlington STATE: Virginia
                                                                                                                                 STREET: 2001 (
STREET: Bldg.
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REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10:
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STREET: Bldg.
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                                                          22202-0286
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: Virginia
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                                                                                                                                              E: Shoemaker and Mattare, Ltd.
2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                             Barenkamp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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703) 415-0813
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                                                                                                                                                                                                                    High Molecular Weight Su
of No. 5603938-Typeable
                                                                                                                                                                                                                                                           Stephen J
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 Mismatches

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Pred. No. 4.9;
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le Haemophilus
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application Patent No. 5869065
GENERAL INFORMATION:
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Best Local 9
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                                   ZIP: 22202-0286

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2469
                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     APPLICANT: BARENKAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2359 ggatttgttcctgaggagatttaatgaaattcagttttgggtc 2401
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NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 16-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US pct/us93/02166
FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel-
CURRENT APPLICATION DATA:
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LENGTH: 4937 base pairs
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APPLICATION NUMBER: GB 9205704.1
                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                 STREET: 2000
Bldg. 1
                                                                                                                                                                          CITY: Arlington
STATE: Virginia
APPLICATION NUMBER:
                                                                                                                                                    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                    ADDRESSEE:
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2001 Jefferson Davis Hwy., 1203 Crystal Plaza
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703) 415-0813
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   US/08/530,198
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Pred. No. 4.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.1%;
Best Local Similarity 50.3%;
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: JWI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,80
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2529 GAACATGAACACAAGCAAACCTTTACCAATTCGGTTTTTAGCC 2571
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NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 16-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 2001 Je
STREET: Bldg. 1
                                                                                                                                                                                                                              CLASSIFICATION:
                NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                       FILING DATE:
                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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VENTION: High Molecular Weight Surface Proteins
VENTION: of No. 5876733-Typeable Haemophilus
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                                                                                                                                                                          16-MAR-1992
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BER: 22,651
NUMBER: 1
                                                                                                                                                                                            GB 9205704.1
                                                                                                                                                                                                                                                                                                 Release #1.0, Version #1.30
                                                                                                                                        US PCT/US93/02166
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1038-516 MIS:vg
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Pred. No. 4.9;
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Best Local Similarity 50.38;
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                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 920
FILING DATE: 16-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
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                                                                                                    ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: 111
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                                                     NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 10
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                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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Bldg. 1
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VENTION: High Molecular Weight Surface Proteins
VENTION: of No. 5928651-Typeable Haemophilus
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101 Jefferson Davis Hwy., 1203 Crystal Plaza
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Pred. No. 4
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US-08-617-697-3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/617,697
FILING DATE: 01-APR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 05-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                        INFORMATION FOR SEQ ID NO:
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LENGTH: 4937 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 4937 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                  FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: 11
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STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                                                                               NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Arlington
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                    TOPOLOGY:
                                  STRANDEDNESS: single
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   TYPE:
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Conservative
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703) 415-0813
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DNA (genomic)
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; Pred. No. 4.9;
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US-08-038-682-6
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Best Local
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Best Local
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 16-MAR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                             2849 CAAAGGCTTAACAACACAGTATAGAAGCTCTGCAGGGGTGAATTTTAACGGCGTAAATGG 2908
                                                                2239 caaagatttagcataccagatgacaatttatgattgggaactcttcaactgcgtgcatga 2298
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2299 gctggagctaatctatcacacatttggaaggcataattttaaaaagaccacagcaaactt 2358
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SOFTWARE: PatentIn Palarring
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STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
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stimulating or suppressing activity, tissue growth activity, chemotactic/chemokinetic activity, chemotactic/chemokinetic activity, chemotactic/chemokinetic activity, activity, receptor/ligand activity, activity, receptor/ligand activity, activity. The polynucleotide may a sequence 335 BP; 118 A; Score t Local Similarity 55.3%; Score t Local Similarity 55.3%; Prediches 120; Conservative 0; Mi 582 tgatagagatagaaaataccaccataag	(GEMY) GENETICS INST INC. Agostino MJ, Jacobs K, Lavallie ER, McCo Racie LA, Spaulding V, Treacy M; WPI, 99-070077/06. New polynucleotides encoding human secre e.g. human blood, kidney, foetal lung, r ovary, pituitary, retina and colon cDNA Claim 1; Page 530-531; 618pp; English. The present sequence represents a human The polynucleotide, which is a secreted are predicted to have useful biological them suitable for treating, preventing o conditions in humans and animals, althon given. Suggested activities include nut:	stand 1999 ne Di secrit grow grow r; l r; l r; l r; l r; l l grow l g l g grow l g l g grow l g l g g g g g l g g g l g g l g g g g g g g g g g g g g g g l g	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
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Sequence 4062 BP; 937 A; 1194 C; 1147 G; 784 T;
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P-PSDB; R91597.
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T13347;
26-JUL-1996 (first entry)
C3G protein gene.
C3G: ras protein guanine nucleotide.
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Claim 2; Page 6; 9pp; Japanese
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28-FEB-1995.
13-JUN-1994; 130699.
11-JUN-1993; JP-140806
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of V21209 from base 1200001 (Methanococcus jannaschii circular
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                  18-DEC-1997;
06-JUN-1997;
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restencsis; AIDS;
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US-048881

US-048884

US-048893

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PR 05-SEP-1997, US-057638.
PR 05-SEP-1997, US-057647.
PR 05-SEP-1997, US-057647.
PR 05-SEP-1997, US-057661.
PR 05-SEP-1997, US-068878.
PR 06-UNN-1997, US-067662.
PR 06-UNN-1997, US-067663.
PR 06-UNN-1997, US-06
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding human secreted proteins (W88534 to W88756). The secreted protein CC gene sequences are deposited with the ATCC under deposit numbers ATCC CC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010, CC 209011, 209080, 209081, 209082, 209083, 209084, 2090885, 209511. Host CC cells comprising recombinant vectors containing the nucleic acid consequences are used for the recombinant production of the secreted cc useful for preventing, treating or ameliorating medical conditions e.g. Cb yroteins The polynucleotide and amino acid sequences are useful for are useful for preventing, treating or ameliorating medical conditions e.g. Cc by determining the amount of the new polynptides in a sample or by determining the presence of mutations in the new polynucleotides. CC specific uses are described for each of the polynucleotides, based on this tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood cdisorders, developmental abnormalities and foetal deficiencies, blood cdisorders, hepatic and renal diseases of the immune system, autoimmune ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, crestenosis, prostate diseases, lymphomas, inflammation, allergies, cschemic shock, Alzheimer's and cognitive disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of testes, lung or thymus, digestive/endocrine disorders, infections and AIDS. The present sequence represents a gene encoding a human secreted protein (see descriptor line for gene number and clone identification).
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W09321314-A.
28-OCT-1993; F00382.
19-APR-1993; F00382.
21-APR-1992; FR-004827.
(RHON) RHONE POULENC RORER S
Schweiahoffer F, Tocque B;
WPI; 93-351724/44.
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Q51233;
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/product= Peptide which
the p21-GDP comm':
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptide(s) modulating GDP exchange in complexes - with ras protein and derived antibodies, nucleic acid etc. esp. for diagnosis and treatment of cancer Claim 5; Page 16-20; 46pp; French.

The peptide(s) encoded by the sequence antagonise the interaction of GDP-exchange factor (GRF) with the p21-GDP complex and thereby regulate the activity of ras gene products. They can also be used to identify other compounds which can modulate GDP exchange. The coding sequence can be used to produce antisense products which can inhibit oncogene expression and for use in diagnosis e.g. detecting (over)expression of GRF for typing of cancers.

Sequence 2652 BP; 706 A; 757 C; 629 G; 560 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2021
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                                                                               Sequence corresp. to the g. in clone SIV-1
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                                                         pSIV-1.1; pSIV-1.2; STLV-III Mac 142-83; Simian immunodeficiency virus.
                                                                                                                   N80860;
15-NOV-1990 (first
                                                                                                                                                N80860
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Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                  gcaagttcaagaagttctatgcggagtttgaaagtttaatggacccttcaaggaaccaca
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                                                                                                                                                                                                                                                                                                                                                AGAATCTCAGAGAAGCTTTGAAAAATTGTGACCCACCCTGTGTCCCTTACCTGGGGATGT
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                                                                                                                                                                                                                                                                                     ACCTCACCGACCTGGCCTTCATCGAGGAGGGGACGCCCAATTACACGGAAGACGGCCTGG
                                                                                                                                                standard;
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                             Location/Qualifiers 551. .2068
                                                                                                                                                  cDNA;
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Pred. No. 2
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                                                                                                      of SIV isolate
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gttcttttgcaacagttcaatacgggcgatgagagagccca

ttggagaagattgtcaagcaaatctcagaagatgcaaaaggcaccacaaaaagaagcacaag 1855 TTGGAGGCAAATATAACGGCCCTCCTAGAAGAGGCACAAATTCAACAAGAGAAGAACATG

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SCOCCOCCOCCOCOPTARRETTE PERETE PERETE POR CORRESPONDE CON CONTRA 
                                                                                                                                                                         pr having the structure of similar immune deficiency virus proteins, provided the structure of similar immune deficiency virus proteins, provided the structure of similar immune deficiency virus proteins, provided the structure of similar immune deficiency virus proteins, and separate of the claim 23; Fig 1B; 86pp; French.

Provided the structure of similar immune deficiency virus proteins, and separate on 15/4/87 at claim 23; Fig 1B; 86pp; French.

Provided the contained in lambda SIV-1 which was deposited on 15/4/87 at the contained is contained in lambda SIV-1.), It is the contained the sequence inserted into a vector are claimed. Labelled fragments of communological properties in common with those of the peptides which have immunological properties in common with those of the peptide skeleton of the envelope protein of HIV-2 and also have a peptide structure in common with that of SIV-1 glycoprotein are claimed. Antigenic and immunogenic configurates contg. the peptides are useful for in vitro diagnosis of HIV-2 infection and some of them can be used as components of immunogens and configurate contained. The sequence is the manual form the sequence in contained in the sequence is sequenced to the sequence in the sequence is sequenced.
Query Matc
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p81759, p81760, p81761, p81762.
New peptide(s) with immunological properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INSP) Inst Pasteur(ALIZ/).
Alizon M, Montagnier L, Gue
Tiollais P, Chakrabarti L,
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                                                                                                vaccines against HIV. Antibodies raised treatment of AIDS.
Sequence 9601 BP; 3277 A; 1809 C;
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15-APR-1987; FR-005398,
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28-JUL-1988
                          Match
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8569. .9354
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/gene="art1"
6090. .8297
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6014. .6130
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/gene="pol"
4826. .5467
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8298. .8732
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Score 35.4;
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                                                          RESULT
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Matches 70
          T37405 standard; cDNA; T37405;
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This nucleotide sequence comprises a cDNA clone coding for Schizosaccharomyces pombe ZRP1 (see W38456), a novel protein that
                                                                                                                                                           2090 GGACTTGA 2097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               renal failure.
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Davis RJ, Galcheva-Gargova
WPI; 98-042192/04
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Schizosaccharomyces pombe RNA-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              increase tubular regeneration of kidney cells, e.g. following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-1997; U09911
06-JUN-1996; US-019
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70; Conserv
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Pred. No. 4.9;
0; Mismatches
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Best Local S
Matches 70
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15-JAN-1992
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Q В Ş В Ωy

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C Prostate timour inducing gene-1 (PTI-1) (T37405) is a novel putative concogene that may contribute to carcinoma development in human prostate and other tissues. PTI-1 was initially identified in the human prostate and other tissues. PTI-1 was initially identified in the human prostate carcinoma LNCaP cell DNA-transfected tumour-derived murine CREF-Trans 6 cells using an RNA differential display method, and full-length cDNA can be directly cloned from an LNCaP cDNA can drull-length cDNA can be directly cloned from an LNCaP cDNA can comprises a unique 5 (330 bp region and can a full-length comprises a unique 5 (330 bp region and can constate and mutated elongation factor-1 alpha gene. It codes for a 46 kDa protein (W03518). PTI-2 (T37412), PTI-3 (T37413) cand a prostate carcinoma tumour antigen gene (T37414) were also clonentified. The PTI-1 gene can be used to design probes useful ce.9. for detection of metastatic cancer, or to produce recombinant proteins. Antisense sequences can be used in cancer therapy. Sequence 2128 BP; 608 A; 434 C; 536 G; 550 T;
                                                                      15-JAN-1992 (first entry)
N.clavipes dragline silk protein coding sequence protein superfibre; major ampullate silk; orb wel
                                                                                                                                                                                                            Q14183 standard; cDNA; 2338
                                                            Nephilia clavipes.
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18-JUL-1996.
11-JAN-1996; U00307.
11-JAN-1995; US-371377.
(UYCO) UNIV COLUMBIA NEW YORK.
Fisher PB, Shen R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding prostate carcinoma tumour antigen and prostate tumour inducing genes - and related proteins, vectors, antibodies, etc., for diagnosis antibodies of metastatic cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prostate tumour inducing gene PTI-1.

Prostate tumour inducing gene-1; PTI-1; oncoger elongation factor-1 alpha; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 8A; 169pp; English.
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                                                                                                                                                                                                                                                                                                                                                                     GCTGCTTTG 1701
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/note= "L
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/note= "A p
621. .1817
Location/Qualifiers
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/note= "ACC encodes Thr"
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Pred. No. 4.
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                                                                                  orb web spider;
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RESULT
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Best Local
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Spider; Nephila clavipes; silk
cocoon; tensile strength; elast
Nephila clavipes
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20-APR-1990; US-511792.
20-APR-1990; US-511792.
(UYWY-) UNIV OF WYOMING.
Lewis RV, Xu M, Hinman M;
WPI; 91-312199/43.
P-PSDB; R14308.
                                                                                                                                                                                             US5728810-A.
17-MAR-1998.
19-APR-1995; 425069.
15-APR-1991; US-684819.
20-APR-1999; US-511792.
04-OCT-1994; US-317844.
19-APR-1995; US-425069.
(UYWY-) UNIV WYOMING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding spider silk protein-1 and 2 and variants - isolated from Nephila clavipes, for prodn. of spider silk protein and fibres having desired characteristics Claim 4; Page 23; 48pp; English.

A N.clavipes major ampullate gland cDNA library was screened with probes based on peptide fragments of the purified spider silk protein (see Q14185). Positive plaques were identified and the spider silk protein coding sequence was determined. See also Q14184.
          Recombinant spider silk proteins - useful for making fibres Recombinant spider silk proteins - useful for making fibres Recombinant spider silk protein from the present invention. Spider silk proteins, and peptide fragments within the proteins, can be produced and purified independently and can then be mixed and made into fibres that have higher tensile strengths and elasticity than naturally occurring fibres. The fibres can be used in mixed composites. The invention allows the two naturally occurring weightle clavipes silk proteins to be produced independently so that they can later be combined to form silk fibres of high tensile strengths.
                                                                                                                                                       Hinman MB, Lewis RV, Xu WPI; 98-270437/24. P-PSDB; W53346.
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85; Conserv
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RESULT 1
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Matches 85
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P-PSDB; W81975, W81976.

New isolated granulcytic erhlichia nucleic acids - used to products for use in vaccines for inhibiting Ehrlichiosis an in detection and diagnosis

in detection and diagnosis.

Claim 2; Fig 1; 184pp; English.
                                                                                                                                                                        This sequence encodes two proteins which are associated with granulocytic ehrlichia (GE), W20.1 and W20.2 which have been isolated from HL60 cells infected with Ehrlichia sp. GE is an acute potentially fatal tick borne infection and the proteins described in this invention can be used in vaccines to elicit a beneficial immune response in an animal to GE. They can be used for inhibiting Ehrlichoisis in an animal to GE. They can be used for detection and diagnosis. Sequence 4833 BP; 1484 A; 797 C; 1114 G; 1438 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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05-NOV-1998.
24-APR-1998; U08264.
25-APR-1997; US-044869.
(AQUI-) AQUILA BIOPHARMACEUTICALS BELTZ G, COUPHIN RT, MURPHY C, ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAR-1999 (first entry)
Ehrlichia sp. W20 genomic Di
Granulocytic ehrlichia; GE;
 4048
                         1145
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               aagggtgtggtctgcaccctgcatgaaggagatgacttcggcaagttagcact
                                                                    gaagaaggtacctcctggtacattattctaaaaggatcagtgaatgtagtcatttacggc 1144
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AGGGATATGCTCTACAACTTCCATTAAGGTGATGATATCGTAAGAAGAACACT
                                                    GAAAAGCATACCTCCAGGTTTCAGTAACTTACAGGAGCTAGATAAAAATTCAGTCAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocytic ehrlichia; GE; W20; tick-borne infection; fatal; vaccine; response; detection; diagnosis; Ehrlichiosis; ss.
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                                                                                                         64; Conservative
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that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S. aureus infection. The polypeptides can also be used in a kit for the immunodetection of S. aureus in a sample. S. aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences
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05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SC
                                                                                                                                                                                                                                                                                                                                                                             (and their fragments) are useful as homologues of any of the S.aureus DN computer readable medium. Sequence 22243 BP; 7693 A; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide(s) and
                                                                                                                                                                                                                                                      1 gatccagcgaagatgtggatataatcttcactcgactgaaagaagttaaagcttttgaga
                                                                                                                                                                           aatttcacccaaatctccttcatcagatttgcttatgtggttattatgagaatctggaaa
                                                                                                                agggaataacattatttcgccagggtgatatgg
                                                                                                                                                    AATGACAAAAGACTATCCTGATCCAGAGTTGTTAATTCGTACTTCAGGAGAACAAAGAAT
                                                                                                                                                                                                                       GCTTCATCAACAAGGTTTAAATAGTGATATCATAGATGAAACATATATAAACAATCATTT
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screening; CDNA

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A (UMIS ) UNIV MISSISSIPPI MEDICAL CENT.

I Ivanov TR, Piletz JE;

WPI; 97-448631/41.

R P-PSDB; W43396.

R P-PSDB; W43396.

R P-PSDB; W43396.

To screening for (ant)agonist, homologous receptors, etc.

Claim 10; Pages 49-50; 72pp; English.

Claim 10; Pages 49-50; 72pp; English or 298 (breakdown product)

This sequence represents cDNA encoding a human imidazoline type 1

Creceptor (IR1), which has 559 (full length) or 298 (breakdown product)

Camino acid residues. The protein is highly unique in its sequence and

Camay represent the first in a novel family of receptor proteins. The cDNA

Can be used to produce recombinant IR1, to screen for ligands binding

IR1, to raise antibodies against IR1 or to probe for other genes encoding
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Best Local &
Matches 98
                                                                                                11-MAR-1999.
03-SEP-1997; U15695.
03-SEP-1997; WO-U15695.
(UMIS ) UNIV MISSISSIPPI MISSISS
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04-SEP-1997.
28-FEB-1997; 1
20-MAY-1996; 1
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Sequence
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   polynucleotides encoding imidazoline receptive polypeptides
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DB; Y05243.
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1677 BP;
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US-650766.
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Pred. No. 4.3;
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1610. .612, aa:Trp)
1646. .648, aa:Trp)
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IVANOV TR, PÍLETZ JE;
WPJ: 97-448631/41.
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This sequence encodes an imidazoline receptor of the invention. Host cells expressing the polypeptides are useful for screening for ligands of an imidazoline receptor. Restriction fragments of the polypurcleotide are useful as labeled probes for isolating and identifying DNA material encoding polypeptides that are receptive to imidazoline compounds. The isolation of polypucleotides encoding the imidazoline receptive polypeptides have immunological and ligand binding properties, which enable identification of agents having greater potency and/or more selectivity for these receptors.

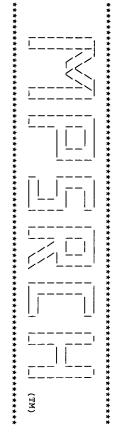
Sequence 1954 BP; 367 A; 645 C; 591 G; 351 T;
Nucleic acid encoding imidazoline receptor subtype screening for (ant)agonist, homologous receptors, e Claim 11; Pages 50-52; 72pp; English.
This sequence represents cDNA encoding a human imid receptor (IR1), which has 559 (full length) or 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human imidazoline receptor subtype 1 Imidazoline receptor subtype 1; IR1; antibody; C-terminal fragment; ds.
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Claim 2; Page 59-60; 1
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                                                                                        2211
                                                                                                                                                               2151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid residues. The protein is highly unique in its sequence and may represent the first in a novel family of receptor proteins. The cDNA can be used to produce recombinant IRL, to screen for ligands binding IRL, to raise antibodies against IRI or to probe for other genes encoding homologous IRI proteins.

Sequence 3317 BP; 721 A; 961 C; 948 G; 687 T;
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                                                                                                                                                                                                                                                                                                  2031 CAGGGCGAGGAGGATGAGGAGGAGGAGGAGGAGGACGTGGCTGAGAACCGCTAC 2090
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Apr 22 13:20:48 2000; MasPar time 123.15 Seconds 477.985 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-09-422-999-18 (1-849) from US09422999.pep 6222

Scoring table: Sequence: PAM 150 Gap 11 1 MVLWKRALTMTGFLTRRTHL.....VIDNQRTLSQMSHRLEPRRP 849

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptrembl12 1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 53.509; Variance 96.380; scale 0.555

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 2 3 3 4 4 4 4 4 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1	Result
6038 5835 30535 2942 2942 1772 595 595 383 370 351 370 320 320 320 320 320 320 320 320 320 32	Score
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CAMP-REGULATED GUANINE CAMP-DEPENDENT RAP1 GUANINE-MUCLEOTID RAP1 GUANINE-MUCLEOTID RAP1 GUANINE-MUCLEOTID CAMP-REGULATED GUANINE CAMP-REGULATED GUANINE MYELOBLAST KIAA0277. KIAA0313 PROTEIN. T14G10.2 PROTEIN. T14G10.2 PROTEIN. AIMLESS RASGEF. 'C3G PROTEIN' KIAO01LB (FRAGMENT). RAS-GPF2 (FRAGMENT). RAS-GPF2 (FRAGMENT). RAS-GRF2 (FRAGMENT). RAS-GRF2 (FRAGMENT). RAS-SPECIFIC GUANINE NUCLEOTIDE EXC RAS-SPECIFIC NUCLEOTID RAS-SPECIFIC NUCLEOTID RAS-SPECIFIC NUCLEOTID CAMP DEPENDENT PROTEIN L	Description
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21	204	w w	689	4	094931	KIAA0846 PROTEIN.	5.52e-16
22	197	3.2	133	σ	077795	E	.98e-
23	192		411	N	083127	CYCLIC NUCLEOTIDE BIND	7.73e-14
24	192		538	ω	Q06729	MAT LOCUS GENES BUD5,	7.73e-14
25	194	3.1	2052	11	Q9Z1T6	FYVE FINGER-CONTAINING	3.42e-14
26	184		581	σ	Q17869	SIMILAR TO CAMP-DEPEND	1.96e-12
27	185			4	Q15300	RET TYROSINE KINASE/CA	1.31e-12
28	180	2.9		4	000538	F25B3.3 KINASE LIKE PR	9.71e-12
29	172	2.8		σı	Q9XTM6	CAMP-DEPENDENT PROTEIN	2.28e-10
30	175	2.8		S	Q25114	REGULATORY SUBUNIT OF	7.02e-11
31	175	2.8		2	P74736	CAMP PROTEIN KINASE RE	7.02e-11
32	177	2.8		5	Q19770	F25B3.3 PROTEIN.	
ω	176	2.8		11	Q9Z1S3	RAS ACTIVATOR RASGRP.	4.74e-11
34	176	2.8		11	088469	RAS GUANYL RELEASING P	4.74e-11
35	176	2.8	797	4	095267	CALCIUM AND DAG-REGULA	4.74e-11
36	167	2.7	325	ഗ	Q94725	44 KDA REGULATORY SUBU	1.59e-09
37	165	2.7	867	G	044235	HRSH2.	3.43e-09
38	162	2.6	224	N	083286	CATABOLITE GENE ACTIVA	1.08e-08
39	154	2.5	678	ഗ	096777	CYCLIC NUCLEOTIDE AND	2.19e-07
40	156	2.5	945	υ	Q9Y1J9	PUTATIVE VOLTAGE-AND C	1.04e-07
41	147	2.4	1048	N	005884	HYPOTHETICAL 110.2 KD	2.87e-06
42	146	2.3	596	σ	Q21758	SIMILARITY TO REGIONS	4.13e-06
43	143	2.3	619	N	067874	HYPOTHETICAL 71.2 KD P	1.22e-05
44	144	2.3	1080	σ	Q23089	ZK742.1 PROTEIN.	8.50e-06
5	145	2.3	1327	4	060859	NEUROPATHY TARGET ESTE	5.93e-06

ALIGNMENTS

K 479	Db 420 DFGKLALVNDAPRAASIVLREDNCHFLRVDKEDFNRILRDVEANTVRLKEHDQDVLVLEK	U
b 257	Qy 198 LSTTVKRELAGVLIFESHAKGGTVLFNQGEEGTSWYIILKGSVNVVIYGKGVVCTLHEGD	Ø
D 419	Db 360 LSTTYKRELAGYLIFESHAKGGTYLFNQGEEGTSWYIILKGSYNYYIYGKGYYCTLHEGI	D.
Н 197	Qy 138 PTEEEKKECDEELQDTMLLLSQMGPDAHMRMILRKPPGQRTVDDLEIIYEELLHIKALSH	0
н 359	Db 300 PTEEEKKECDEELQDTMLLLSQMGPDAHMRMILRKPPGQRTVDDLEIIYEELLHIKALSH	D.
L 137	Qy 78 ELVDWMIDETPCVHSRTQAVGMWQVLLEDGVLNHVDQEHHFQDFYLFYRFLDDEHEDAPL	Ø
L 299	Db 240 ELVDWMMQQTPCVHSRTQAVGMWQVLLEDGVLNHVDQEHHFQDKYLFYRFLDDEHEDAPL	D.
T 77	Qy 18 THLIEPHVPLRPANTITKVPSEKILRAGKILRNAILSRAPHMIRDRKYHLKTYRQCCVGT	Ю
T 239	Db 180 TPLIEPHVPLRPANTITKVPSEKILRAGKILRNAILSRAPHMIRDRKYHLKTYRQCCVGT	D.
Gaps 0;	Query Match 97.0%; Score 6038; DB 4; Length 1011; Best Local Similarity 99.4%; Pred. No. 0.00e+00; Matches 827; Conservative 3; Mismatches 2; Indels 0; G6	
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	DR EMBL; U78516; AADU3422.1; DR HSSP: P00515: 2BPK.	ם ם
	Science 282:2275-2279(1998).	×
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	RA KAWASAKI H., SPRINGETT G.M., MOCHIZUKI N., TOKI S., NAKAYA M., RA MATSUDA M., HOUSMAN D.E., GRAVBIET A M.:	z z
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Matches 79
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Q9Z1P0;
Q9Z1P0;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-MAY-1999 (TrEMBLrel. 12, Last annotation update)
Q1-MOV-1999 (TrEMBLRel. 12, Last annotation update)
CAMP-DEPENDENT RAP1 GUANINE-NUCLEOTIDE EXCHANGE FACTOR
MUS musculus (Mouse).
                                                                                                                                                                                                                                                                                                                         SEQUENCE
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musculus (Mouse).
aryota; Metazoa; Chordata; Craniata; Vertebrata;
heria; Rodentia; Sciurognathi; Muridae; Murinae;
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                  KAWASAKI H., SPRINGETT G.M., M
MATSUDA M., HOUSMAN D.E., GRAY
"A family of CAMP-binding prot
Science 282:2275-2279(1998).
EMBL; U78517; AAD03423.1; -.
NON_TER 1 1
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Q9Z1C7;
Q9Z1C7;
Q9Z1C7;
01-MAY-1999 (TrEMBLrel. 1
01-MAY-1999 (TrEMBLrel. 1
01-MAY-1999 (TrEMBLrel. 1
CAMP-REGULATED GUANINE NU
                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
MEDLINE; 99074384.
                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                        Eutheria;
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. 10, Last sequence update)
. 10, Last annotation update)
NUCLEOTIDE EXCHANGE FACTOR II
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DE ROOIJ J., ZWARTKRUIS F.J.T., VI
NIJMAN S.M.B., WITTINGHOFER A., BC
"Epac is a Rapl guanine-nucleotide
by cyclic AMP.";
Nature 396:474-477(1998).
EMBL; AF103905; AAC83381.1; -.
HSSP; P00515; 2BPK.
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095398;
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01-MAY-1999 (
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
RAP1 GUANINE-NUCLEOTIDE EXCHANGE FACTOR.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
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larity 95.6%;
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Pred. No. 0.00e+00;
189; Mismatches 188
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Pred. No. 0.00e+00;
10; Mismatches 9;
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01-MAY-1999 (TrEMBLrel. 1(
01-NOV-1999 (TrEMBLrel. 1(
01-NOV-1999 (TREMBLREL. 1)
Query Match
Best Local Similarity
                           KAWASAKI H., SPRINGETT G.M.,
MATSUDA M., HOUSMAN D.E., GRR
"A family of cAMP-binding pro
Science 282:2275-2279(1998).
EMBL; U78168; AAD12740.1; -.
HSSP: PO0515; 2BPK.
SEQUENCE 881 AA; 99376 MW.
                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; C:
Eutheria; Primates; Catarrhini;
                                                                                                                                                 CAMP-GEFI
                                                                                        SEQUENCE FROM N.A. MEDLINE; 99074384.
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. 10, Last sequence update)
. 12, Last annotation update)
NUCLEOTIDE EXCHANGE FACTOR I
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, GRAYBIEL A.M.;
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Pred.
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2936; DB 4;
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                                     Eukaryota;
Eutheria; F
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2 IANTARTVRYYRSQ
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                                                                                                                                                                                                                                                         CSQLSKRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSRLALTWEKLPSKFKKFY
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                                                            norvegicus (Rat).
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  99074384.
                                       Rodentia;
                                                 Metazoa;
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                                    Chordata; Craniata; Ve
Sciurognathi; Muridae;
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                                     Vertebrata;
ae; Murinae;
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Matches 4(
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"A family of camp-binding proteins that directly Science 28:2275-2279(1998).
EMBL; U78167; AAD12739.1; -.
HSSP; P00515; ZBPK.
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                                                                                                                                                                                                                                                                                                                                                                                                                LERTSQGA-GPSRPPTPGRNRYTVMSGTPEKILELLLEAMRPDSSAHDPTETFLSDFLLT
                       MRMMARAVRMLHHCRSHSTAP
                                                                                               MRMIANTARTVRYYRSOPFNP
                                                              KLYSALERLLDPSWNHRVYRLALTKLSPPVIPFMPLLLKDMTFIHEGNHTLVENLINFEK
                                                                                                                                                                                                                                                                                                                SDPVATSFLQKLSDLVSRDTRLSNLLREQYPERRRHHRLENGCGNVSPQTKARNAPVWFP
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                                                 KFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFMPLLIKDMTFTHEGNKTFIDNLVNFEK
                                                                                                                                                                                              VKMSSGGEKVYLKPNDVSVFTTLTINGRLFACPREQFDSLTPLPEQEGPTVGTVGTFELM
                                                                                                                                                                                                              VKVNSAGDVVGLQPDARGVATSLGLNERIFVVDPQEVHELTPHPEQLGPTLGSSEMLDLV
                                                                                                                                                                                                                                                                                                   EDDVSMAFLEEFYVSVSDDARMIAALKEQLPELEKIVKQISE-DAKAPQKKHKVLLQQFN
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ilarity 50.1%;
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Pred. No. 0.00e+00;
186; Mismatches 200;
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01-FEB-1997 (TrEMBLrel. 01-NOV-1998 (TrEMBLrel. MYELOBLAST KIAA0277. KIAA0277.

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TISSUE-BRAIN;

SEQUENCE FROM N.A.

Matches Query Match

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Conservative

Local Similarity

PEAM; PEUUL... PEAM; PEU0618; RasGE

D87467; BAA13406.1; -. PF00617; RASGEF; 1. PF00618; RASGEFN; 1. NCE 580 AA; 67733 MW;

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EMBL;

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RESULT
ID QS
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                                                                                                                           O9Y4G8 PRELIMINARY;
O9Y4G8;
O1-NOV-1999 (TIEMBLIEL 1
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O1-NOV-1999 (TIEMBLIEL 1
KIAAO313 PROTEIN.
KIAAO313;
       Eukaryota; Metazoa;
                                                                 Homo sapiens (Human)
       Chordata;
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       Craniata;
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              Vertebrata;
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NAGASE T., SEKI N., ISHIKAWA K., OHIRA M., KAWARABAYASI Y., TANAKA A., KOTANI H., MITAJIMA N., NOMURA N., "Prediction of the coding sequences of unidentified human get the coding sequences of 80 new genes (KIAA0201-KIAA0280) decanalysis of cDWA clones from cell line KG-1 and brain."; DNA Res. 3:321-329(1996).
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primaces; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                   DAAQANKNHODVRSYVRQLNVIDNORTLSOMSHRLEPR
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47.3%; Pred. No. 0.00e+00;
rvative 125; Mismatches 138;
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O21218; Q22503;
O1-NOV-1996 (TrEMBLrel. 0:
O1-MAY-1999 (TrEMBLrel. 1:
O1-MAY-1999 (TREMBLrel. 1:
T14G10.2 PROTEIN.
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"Prediction of the coding sequences of unidentified human genes The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 4:141-150(1997).
EMBL; AB002311; BAA20772.1; -.
SEQUENCE 1499 AA; 167416 MW; D7CB0593 CRC32;
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Eukaryota; Metazoa; Nemato
Rhabditina; Rhabditoidea;
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EMBL; Z68880; CAA93519.1; JOINED.
EMBL; Z68880; CAA93100.1; -
EMBL; Z69664; CAA93100.1; JOINED.
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78; Mismatches 101;
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DR EMBL; U53884;
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Best Local :
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CUIT. Biol. 6:0-0(0).

EMBL: U53884; AAB09441.1; -

EMBL: U59887; RASGEF 1.

PFAM: PF00618; RASGEFN: 1.

PFAM: PF00618; RASGEFN: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QFWVVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSRLALTWE
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                           of Crk.";
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    (APR-1994)
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larity 27.5%;
Conservative
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Pred. No. 2.36e-51;
67; Mismatches 73;
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Last sequence update)
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Last sequence update)
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Best Local S
Matches 6
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043386;
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MEDLINE; 95105157.
KNUDSEN B., FELLER S., HANAFUSA H.;
"Four proline-rich sequences of the C3G bind with unique specificity to Crk.";
                                                                                                                     CONNOLLY K.S., GUNNING K.M., DAVIS C.A., KADNER K., SUBRAMANIAN S., MIGUEL T., LEWIS K.D., FRIDLYAND J., BALCIVARE D., BENKE J.A., BONDEN E., CRITAND A., CRITZ P., JAKLEVIC M.A., LINDO K., LINDOC M., BOWEN E., CHINGA A., PISCIA C., RILEY B.E., ROJESKI H., LINDOUIST K., MILLER C., PATEL S., PISCIA C., RILEY B.E., ROJESKI H., SARMIENTO R., YU C., MONTENEGRO M., AERTS A., CHUNG A., ABRAJANO A., SARMIENTO R., GAU C., JONNEY J., KO C., BEALL K., WOOLLEY J.P., STULTZ J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
TISSUE=SPLEEN, AND
             SEQUENCE FROM N.A.
RICKE D.O., WAGNER R.P.;
RICKE D.O., WAGNER R.P.;
Submitted (FEB-1998) to the
EMBL; AC004227; AAC04379.1;
HSSP; P31016; 1BFE.
                                                                                                                                                                                                                            Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                             1007
                                                                                                             BAKER M., GAKIMMERLY W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 94211880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem.
                                                                                                 Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WVRSIIMLQEKAQDRERLLLKFIKIMKHLRKLUNFNSYLAILSALDSAPIRRLE--WQKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTLHDFHSHEIAEQLTLLDAELFYKI-EIPEVL-LWAKEQNEEKSPNLTQFTEHFNNMSY
                                                                                                                                                                                                                                                                                                                                                                                                                                            VNFSKRWQQFNILDSMRCFQQAHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSE--GL-AEYCTLIDSSSSFRAYRAALSEVEPPCIPYLGLILQDLTFVHLGNPDYIDGK 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                      VNFEKMRMIANTARTVRYYRSQPFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSKFKKFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFMPLLIKDMTFTHEGNKTFIDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WVVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSRLALTWEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a guanine nucleotide-releasing protein expressed ubiquitously, to the Src homology 3 domains of CRK and GRB2/ASH proteins.", Natl. Acad. Sci. U.S.A. 91:3443-3447(1994).
D21239; BAA04770.1; -.
PF00617; RASGEF; 1.
PF00618; RASGEFN; 1.
  PF00027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 69; Conser
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                                                                                              W., MARTIN C.H.
(FEB-1998) to
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larity 33.7%;
Conservative
cNMP_binding;
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                                                                                              EMBL/GenBank/DDBJ
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Last annotation update)
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Pred. No. 1.20e-48;
52; Mismatches 77;
                                          EMBL/GenBank/DDBJ
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the first Src homology
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logy 3 domain
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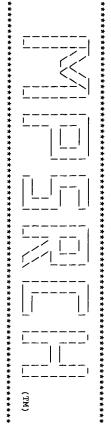
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Best Local Similarity 26.9%;
Matches 66; Conservative
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Best Local Similarity 32.8%;
Matches 60; Conservative
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014827
014827;
014827;
01-JAN-1998 (TYEMBLIEL 05, C
01-JAN-1998 (TYEMBLIEL 05, C
01-MAY-1999 (TYEMBLIEL 10, L
RAS-GRE2 (FRAGMENT)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                     998 FESLSAMELAEQITILDHVIFRSIPYEEFIGQGWMKLDKNERTPYIMKTSQHFNDMSNLV 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134
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; PF00618; RASGEFN; 1.
; PF00621; RhoGEF; 1.
TER 1237 1237
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     EPRRP
                                                  EPRLP 1236
                                                                                                                                                                                                KFKKFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFMPLLIKDMTFTHEGNKTFIDN-LV
                                                                                                                                                                                                                                                QTKALMDKLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAFIEEGTPNFTEEGLV
                                                                                                                                                                                                                                                                                                                                                                                                FELMSSKDLAYQMTIYDWELFNCVHELELIYHTFGRHNFKKTTANLDLFLRRFNEIQFWV
                                                                                                  NFEKMRMIANTARTVRYYRSQPFNPDAAQANKNHQDVRSYVRQLNVIDNQRTLSQMSHRL
                                                                                                                                                NFSKMRMISHIIREIRQFQQTSYRIDH-QP-KVAQYLLD--KDL-IIDED-TLYELSLKI 1231
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PF00612; IQ; 1.
PF00169; PH; 2.
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579 AA;
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65197 MW;
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Pred. No. 1.32e-39;
72; Mismatches 100; Indels
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Pred. No. 1.02e-44;
56; Mismatches 61; Indels
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RESULT 14

P70392;
AC 970392;
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DT 01-FEB-1997 (
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DE RAS PROTEIN-S
DE (RAS-GKF2).
GN RASGRF2.
OS MUS MUSCULUS
OC EURARYOTA; MO
COC EUTHORIA; RO
RT SEQUENCE FROM
RC 115SUE-BRAIN;
RX MEDLINE; 9412
RA CHEEL, ZHAN
RT "A MUTINE COC
RT regulation.";
RL Dev. Genet. 1
RN [2]
RN EZUE-BRAIN;
RX MEDLINE; 9714
RA TAM N.P., PAN
RT TISSUE-BRAIN;
RX MEDLINE; 9714
RA FAM N.P., FAN
RT TESUE-BRAIN;
RX MEDLINE; 9714
RA FAM N.P., FAN
RT TESUE-BRAIN;
RX MEDLINE; 9714
RA FAM N.P., FAN
RY MEDLINE; 9716
RP SEQUENCE FROM
RC TISSUE-BRAIN;
RX MEDLINE; 9716
RP FRAM; PF0061:
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Best Local 9
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O15059;
O1-JAN-1998
O1-JAN-1998
O1-NOV-1998
KIAA0351.
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PFAM; PF00169; PH; 2.
PFAM; PF00617; RasGEFY,
PFAM; PF00618; RasGEFY,
PFAM; PF00621; RhoGEF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and characterization of Ras-GRF2, a novel exchange factor for Ras.";
MO1. Cell. Biol. 17:1396-1406(1997).
EMBL; U67326; AAC53058.1; -.
MGD; MGI:109137; Rasgrf2.
PFAM; PF00612; TO: 1
 KIAA0351.
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Modentia; Sciurognathi; Muridae; Murinae;
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CHEN L., ZHANG L.J., GREER P., TUNG P.S., MORAN M.F. "A murine CDC25/ras-GRF-related protein implicated in
                                                                                                                                                                                                                         1184
                                                                                                                                                                                                                                                                                                                                                              1070
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FAM N.P., FAN W., ZHANG L.,
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   sapiens
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Similarity 26.9%;
66; Conservation
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(TYEMBLrel. 02, Last sequence update)
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-SPECIFIC GUANINE NUCLEOTIDE-RELEASING F
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   (Human)
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RasGEFN; 1.
RhoGEF; 1.
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Last sequence update)
Last annotation updat
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Pred. No. 2.17e-38;
71; Mismatches 101;
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Search completed: Sat Apr 22 13:22:56 2000 Job time : 128 secs.
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Best Local Similarity 25.8%;
Matches 64; Conservative
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TISSUE-BRAIN;
MEDLINE; 97349984.
MAGASE T., ISHIKAWA K., NAKAJIWA D., OHIRA M., SEKI N., MIYAJIWA N.,
NAGASE T., ISHIKAWA K., NAKAJIWA D., OHIRA M., SEKI N., MIYAJIWA N.,
PRANAKA A., KOTAWI H., NOMURA N., OHARA O.;
PRANAKA A., KOTAWI H., NOMURA N., OHARA N.,
PRANAKA A., KOTAWI H., NOMURA N.,
PRANAKA N., PRANAKA N.,
PRANAKA N., PANAKA N.,
PRANAKA N., PANAKA N.,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
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                                                                                                                                            839
                                                                                                                                                                                                                                                                             782
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                                                                                                                                                                                       281 KLSLRIEP 288
                                                                                                                                                                                                                                                                                                                                                                                                        NLVNFEKMRMIANTARTVRYYRSQ-PFNP-DA-AQANKNHQDVRSYVRQLNVIDNQRTLS 838
                                                                                                                                            QMSHRLEP 846
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Apr 22 13:19:37 2000; MasPar time 50.95 Seconds
497.627 Million cell updates/sec

Tabular output not generated.

Title: >US-09-422-999-18
Description: (1-849) from US09422999.pep
Perfect Score: 6222

Sequence: 1 MVLWKRALIMTGFLTRRTHL.....VIDNQRTLSQMSHRLEPRRP 849

Scoring table: PAM 150 Gap 11

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38
1:swissprot

Statistics: Mean 55.453; Variance 99.565; scale 0.557

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2222118 2322213 2322213 24322213 2532223	Result
1922 317 310 291 291 278 278 255 255 257 257 253 259 216 210 210 201 201 201 201 201	Score
30000000000000000000000000000000000000	Query Match I
1213 12142 12642 12642 1232 1232 1232 1233 1233 1233 1253 125	Length 1
	DB
YNX5_CAEEL CC25_SACKL GNRP_MOTS GNRP_MOTS STE6_SCHPO SOS2_HOWAN SOS2_HOWAN CC25_CANAL CC25_YEAST SOS_DROME SOS_DROME APR_CAEEL LITE1_YEAST KAPR_DROME KAPR_SOME KAPR_SOME KAPR_SOME KAPR_SCHPO KAPR_SCHPO KAPR_SCHPO KAPR_SCHPO KAPR_VEAST	ID
HYPOTHETICAL 139.4 KD CELL DIVISION CONTROL GUANINE NUCLEOTIDE REL GUANINE NUCLEOTIDE REL STE6 PROTEIN. SON OF SEVENLESS PROTE SON OF SEVENLESS PROTE SON OF SEVENLESS PROTE SON OF SEVENLESS PROTE CELL DIVISION CONTROL CELL DIVISION CONTROL CELL DIVISION FROTEIN CAMP-DEPENDENT PROTEIN CAMP-DEPENDEN	Description
0.00e+00 1.63e-37 4.15e-36 2.51e-32 9.01e-30 1.95e-25 1.95e-25 6.15e-25 6.15e-25 6.16e-25 6.26e-17 6.26e-17 6.26e-17 4.97e-16 7.17e-16 7.13e-15 1.13e-15 1.13e-15 1.13e-15 1.13e-15	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
143	151	153	157	159	162	165	165	166	166	165	166	165	165	171	172	173	177	181	180	180	184
2.3	2.4	2.5	2.5	2.6	2.6	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.8	2.8	2.8	2.9	2.9	2.9	3.0
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GNDS_MOUSE	KAP2_MOUSE	KAPR_COLTR	KAP2_BOVIN	KAPR_EMENI	KAP2_HUMAN	YJ9G_YEAST	KGP2_HUMAN	KGP2_MOUSE	KGP2_RAT	KAP3_BOVIN	KAP3_HUMAN	KAP3_RAT	KAPR_BLAEM	KAPR_NEUCR	KAPO_PIG	KAPR_STRPU	KAPR_DICDI	KAPO_HUMAN	KAPO_RAT	KAPO_BOVIN	KAPR_MAGGR
GUANINE NUCLEOTIDE	CAMP-DEPENDENT	CAMP-DEPENDENT	CAMP-DEPENDENT	CAMP-DEPENDENT	CAMP-DEPENDENT	HYPOTHETICAL 182.0 KD	CGMP-DEPENDENT	CGMP-DEPENDENT	CGMP-DEPENDENT	CAMP-DEPENDENT											
CIDE DIS	PROTEIN	PROTEIN	PROTEIN	PROTEIN	PROTEIN	32.0 KD	PROTEIN														
1.23e-05	7.03e-07	3.39e-07	7.81e-08	3.72e-08	1.21e-08	3.91e-09	3.91e-09	2.68e-09	2.68e-09	3.91e-09	2.68e-09	3.91e-09	3.91e-09	3.96e-10	2.69e-10	1.83e-10	3.87e-11	8.05e-12	1.19e-11	1.19e-11	2.46e-12

ALIGNMENTS

Dβ	Оу	M B Q	DR SQ	455555555555555555555555555555555555555	RR RR RR C OC S	RESULT ID Y AC P DT 0 DT 0 DT 0
474 SRIQMSAIWQVLLNNGLISHIDGEHQFLDKTNSYYRWVQQFRSRNKVAPSIEEV 527	414 EKQIRDSGGILHRKMLTDNHQVIRDITTEHTRVQNCMIGAEMIDWLLTLFVSTSTTCSSL 473 : : : : : : : : : : : : :	Query Match 30.9%; Score 1922; DB 1; Length 1213; Best Local Similarity 38.5%; Pred. No. 0.00e+00; Matches 311; Conservative 204; Mismatches 259; Indels 33; Gaps 24;	EMBL; Z30423; CAAB3013.1; PIR; S42368; S42368. HSSP; P00514; 1BPK. WORMPEP; T20G5.5; CE00479. WORMPEP; T20G5.5; CE00479. PRAM; PF00027; CNMP_BINDING_3; 2. PFAM; PF00610; DEP; 1. PFAM; PF00611; RasGEF; 1. PFAM; PF00618; RasGEF; 1. Hypothetical protein. SEQUENCE 1213 AA; 139379 MW; DB4E0F1E CRC32;	Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases. -I- SIMILARITY: TO CAMP DEPENDENT PROTEIN KINASE REGULATORY CHAIN. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).		YNX5_CAEEL STANDARD; PRT; 1213 AA. P34578; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update) HYPOTHETICAL 139.4 KD PROTEIN T20G5.5 IN CHROMOSOME III.

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               Saccharomyces cerevisiae.";
Gene 117:67-72(1992).
-I- FUNCTION: PROMOTES THE I
                                                                     SEQUENCE FROM N.A.
MEDLINE; 92354938.
PRIGOZY T., GONZALES E., BROE
"Identification and analysis
                                                                                                                                                                                                        01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CCLL DIVISION CONTROL PROTEIN 25 (FRAGMENT).
                                                       PRIGOZY T., GONZALES E., BROEK D.;
"Identification and analysis of a DNA
kluyveri that can complement the loss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1061
                                                                                                                                                                Saccharomyces kluyver1 (Yeast).
Eukaryota; Fung1; Ascomycota; Fung1;
                                                                                                                                                                                                                                                                                  CC25_SACKL
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                                                                                                                                                 Saccharomycetaceae;
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FUNCTION: PROMOTES PROTEIN POSITIVELY
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                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                 Saccharomyces
THE EXCHANGE CONTROLS THE
                                                                                                                                                               Hemiascomycetes;
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OF RAS-BOUND GDP BY GTP. 1
LEVEL OF CELLULAR CAMP AT
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of CDC25
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Best Local S
Matches
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P28818;
01-DEC-1992
01-DEC-1992
15-JUL-1999
               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Rodentia; Sciurognathi; Murid
                                                                                                                                                                                                                                                                               GUANINE NUCLEOTIDE RASGRF1.
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SEQUENCE
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PFAM;
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PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                          MEDLINE; 92350260
                                                                                                                                                                                                          TISSUE=BRAIN;
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitosis; Transmembrane.
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                                                                                                                                                                                 SHOU C., FARUSWORTH C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           665
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PF00618; RasGEFN;
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Conservative
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institutions as long as its content is in:
atement is not removed. Usage h...
                                                                                                                                                                  .L., NEEL B.G., FEIG L.A.;
cDNAs encoding a guanine-nucleotide-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 317; DB 1;
Pred. No. 1.63e-37;
50; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor;
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                                                                                                                                                                                                                                             Muridae;
                                                                                                                                                                                                                                                                                                                    update;
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                                                                                                                                                                                                                                             Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1095
                                                                                                                                                                                                                                                                                            RAS-GRF).
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Rattus.
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MBL outstation -
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PROSITE;
PROSITE;
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01-AUG-1992 (Rel. 23, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).
RASGREI OR CDC25MM OR GREI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM;
PFAM;
PFAM;
PFAM;
MARTEGANI E., VANONI M., ZIPPEL R., COCCETTI P., BRAMBILLA R., FERRARI C., STURANI E.P., ALBERGHINA L.; "Cloning by functional complementation of a mouse cDNA encoding homologue of CDC25, a Saccharomyces cerevisiae RAS activator."; EMBO J. 11:2151-2157(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNRP_
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DOMAIN
                                                                                                                                                         SEQUENCE OF 791-1262 FROM N.A. STRAIN-SWISS; TISSUE-BRAIN;
                                                                                                                                                                                                                        "Isolation of multiple mouse cDNAs with coding Saccharomyces cerevisiae CDC25: identification Bcr, Vav, Dbl and CDC24.";
EMBO J. 11:4007-4015(1992).
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Morazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                 CEN H., LOWY D.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria; Rodentia;
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PS00741; GDS_CDC24;
PS50003; PH_DOMAIN;
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1244 AA;
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"Identification of a mammalian gene structurally and related to the CDC25 gene of Saccharomyces cerevisiae Proc. Natl. Acad. Sci. U.S. A. 89:7100-7104(1992).
-i- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP-i- TISSUE SPECIFICITY: BRAIN.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetace
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PIR; S22693; S22693.
MGD; MGI:99694; RASGRF1.
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SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
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PF00612; IQ; 1.
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PS00741; GDS_CDC24;
PS50003; PH_DOMAIN;
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Pred. No. 2.51e-32;
63; Mismatches 93;
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Best Local
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                                                                                        Eukaryota;
Eutheria; F
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PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Homologous activators of ras in fission and budding yeast.";
Nature 344:355-357(1990).
-I- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP. THIS PROTEIN IS ESSENTIAL FOR MATING.
-I- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
   BAR-SAGI D.;
                MEDLINE; 93262494
CHARDIN P., CAMON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S28098; S28098.
PROSITE; PS00720; GDS_CDC25;
PROSITE; PS50002; SH3; 1.
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                                               TISSUE-BRAIN;
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[1]
                                                           SEQUENCE FROM N.A.
                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Local Similarity 22.2%;
hes 57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            -FKKTTANLDLFLRRFNEIQFWVVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QELEDLS-LHNSPDPIIYKDELVLLLPPREIAKQLCILEFQSFSHISRIQFLTKIWDNLN 696
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                                                                                                                                                                                                                                                                                                                                            PLLIKDMTFTHEGNKTFIDNLVNFEKMRMIANTARTVRYYRSQPFNPDAAQANKNH-QDV
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90190870.
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                  CAMONIS J.H.,
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                  GALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 278;
Pred. No. 9
75; Mismat
                N.W.,
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(SOS-2).
               VAN AELST L.,
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                WIGLER M.
                                                                                                        Mammalia;
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                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 601247; -. PS00720; GDS_CDC25; PROSITE; PS00720; PH_DOMAIN; PH_DOMAIN;
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-1- SIMILARITY: CONTAINS 1 PH DOMAIN.
-1- SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-PLACENTA;
                                                                                                                                                                                                                      SEQUENCE
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[2]
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                                            704
                                                                                                                                                    752 FESPPPPIEWHISKPGQFETFDLMTLDPIEIARQLTLLESDLYRKVQPSELVGSVWTKED 811
PLLIKDMTFTHEGNKTFI---D-NLVNFEKMRMIANTARTVRYYRSQPF
                                          GIYLTNILKTEEGNNDFLKRKGKDLINFSKRRKVAEITGEIQQYQNQPY
                                                                                     FKKTTANLDLFLRRFNEIQFWVVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFFA
                                                                                                        KEINSPNLLKMIRHTTNLTLWFEKCIVEAENFEERVAVLSRIIEILQVFQDLNNFNGVLE 871
                                                                                                                                FDSLTPLPEQEGPTVGTVGTFELMS--SKDLAYQMTIYDWELFNCVHELELIYHTFGRHN
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PF00621; RhoGEF; 1.
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larity 25.8%;
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Pred. No. 1.33e-28;
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MGD; MGI:
PROSITE;
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DOMAIN
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"Identification of murine homologues of the Drosophila sevenless gene: potential activators of ras.";
Proc. Natl. Acad. Sci. U.S.A. 89:6511-6515(1992).
-!- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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-i- SIMILARITY: CONTAINS 1 PH DOMAIN.
-i- SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
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STRATH-SWISS; TISSUE-EYE;
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                                                                              GIYLTNILKTEEGNSDFLKRKGKDLINFSKRRKVAEITGEIQQYQNQPY
                                                                                                  FKKTTANLDLFLRRENEIQFWVVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFFA
                                                                                                                                                                    KEINSPNLLKMIRHTINLTLWFEKCIVEAENFEERVAVLSRIVEILQVFQDLNNFNGVLE
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                                                        PLLIKDMTFTHEGNKTFI---D-NLVNFEKMRMIANTARTVRYYRSQPF
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                                                                                                                                                                                                                                                                                                                                                                                 PF00621;
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Metazoa; Chordata; Prantia; Sciurognathi; א
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             STANDARD;
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PROTEIN HOMOLOG 2 (SOS-2) (MSOS-2) (FRAGMENT).
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70; |
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DOMAIN
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J. Mol. Biol. 269:579-591(1997).
-i- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BOWTELL D., FU P., SIMON M., SENIOR P., "Identification of murine homologues of the Drosophila sevenless gene: potential activators of ras.", Proc. Natl. Acad. Sci. U.S.A. 89:6511-6515(1992).
                                                                                                                                                                                                                                                                  Guanine-nucleotide releasing DOMAIN 202 443
                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long amodified and this statement is not removed.
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STRAIN=SWISS; TISSUE=EYE;
                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                           PFAM; PF00618; RaSGEFN; 1. PFAM; PF00621; RhoGEF; 1.
                                                                                                                                                                                                                                                                                                                PFAM; PF00169; PH; 1.
PFAM; PF00617; RasGEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <del>-</del>
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             932
                                    704
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TISSUE SPECIFICITY: EXPRESSED IN MOST EMBRYONIC SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).

SIMILARITY: CONTAINS 1 PH DOMAIN.

SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute. The by non-profit institutions as long
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                                                                               FKKTTANLDLFLRRFNEIQFWVVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFFA
                                                                                                      KEINSPNLLKMIRHTTNLTLWFEKCIVETENLEERVAVVSRIIEILQVFQELNNFNGVLE
                                    IVMGLSNIAVSRLALTWEKLPSKFKKFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFMP
                                                                                                                                                                                    4.18;
Similarity 25.48;
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letazoa; Chordata; Craniata; Vertebrata;
dentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                    Score 255;
Pred. No. 2.
                                                                                                                                                                                                                       MW; A317F43B CRC32;
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of mouse
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                                                                                                                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           PFAM;
PFAM;
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                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L13857; AAA35913.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                         Guanine-nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZHENG J.,
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SIMILARITY: CONTAINS 1 PH DOMAIN.
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; PF00618; RasGEFN; 1.
; PF00621; RhOGEF; 1.
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                                                                                                                                        WW.
Score 257; DB 1; Le
Pred. No. 1.06e-25;
65; Mismatches 97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOLDBERG D., MARBACH I., GRO
"A Candida albicans homolog cerevisiae.";
                1129
                                                                      1071 ELARQLTLREFKLY-CKITKFACLAKVWGKKSGLSESIDSITQFIKASNQLTNFVGYMI- 1128
                                                                                                                                                                                           Mitosis; SH3 domain.
                                                                                                                                                                                                                                      PROSITE; PS00720; GDS_CDC25; PROSITE; PS50002; SH3; 1. PFAM; PF00018; SH3; 1. PFAM; PF00617; RasGEF; 1.
                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUR. J. BIOChem. 213:195-204(1993).

11- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP. THIS
PROTEIN POSITIVELY CONTROLS THE LEVEL OF CELLULAR CAMP AT START,
THE STAGE AT WHICH THE YEAST CELL DIVISION CYCLE IS TRIGGERED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Candida albicans (Yeast).
Eukaryota; Fungi; Ascomyo
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                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                            Guanine-nucleotide releasing
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PFAM; PF00617; RasGEF; 1.
PFAM; PF00618; RasGEFN; 1
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                                            DLAYOMTIYDWELFNC-VHELELIYHTFGRHN-FKKTTANLDLFLRRFNEIQFWVVTEIC
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1333 AA;
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Rel. 38, Last annotation
CONTROL PROTEIN 25.
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152012 MW;
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Pred. No. 6.15e-25;
60; Mismatches 87
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                                                                                                                                                                                                            Cell division;
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CC25_YEAST STANDARD; PRT; 1589 AA.
P04821;
13-AUG-1987 (Rel. 05, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
CELL DIVISION CONTROL PROTEIN 25.
CDC25 OR CTN1 OR YLK310C OR L2142.6.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                   JOHNSTON M. ANDREWS S., BRINKMAN R., COOPER J., DING H., DE FAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J., KUCABA T., HALLSWORTH K., HAWKINS J., HILLIER L., JIER M., JOHNSON D., JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., JOHNSON D., JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., WARDIS E., MENEZES S., MILLER N., HANN M., PAULEY A., PELUSC RIFKEN L., RILES L., TAICH A., TREVASKIS E., VIGNATI D., WILCOX L., WOHLDMAN P., VAUDIN M., WILSON R., WATERSTON R.; Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                        This SWI
                                                      JONES S., VIGNAIS M.L., BROACH J.R.;
"The CDC25 protein of Saccharomyces cerevisiae promotes exchange of guanine nucleotides bound to ras.";
Mol. Cell. Biol. 11:2641-2646(1991).
-!- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP. THIS PROTEIN POSITIVELY CONTROLS THE LEVEL OF CELLULAR CAMP AT START, THE STAGE AT WHICH THE YEAST CELL DIVISION CYCLE IS TRIGGERED.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                "Characterization, cloning and sequence analysis of the CDC25 which controls the cyclic AMP level of Saccharomyces cerevisia EMBO J. 5:375-380(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The
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POWERS S., WIGLER M.;
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MEDLINE; 89181526.
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                                                                                                                                                          MEDLINE; 91203884.
                                                                                                                                                                       FUNCTION
                                                                                                                                                                                                         mitosis
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                                                                                                                                                                                                      T., MINK M., KUNTZEL H.; s of the Saccharomyces cerevisiae and meiosis.";
                                                                                                                                                                                            Genet.
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Query Match
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PROSITE; PS00720; GDS_CDC25;
PROSITE; PS50002; SH3; 1.
PFAM; PF00018. ST
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P26675;
01-AUG-1992
01-AUG-1992
15-JUL-1999
SEQUENCE FROM N.A. MEDLINE; 92034991. SIMON M.A., BOWTELL "Ras1 and a putativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
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TRANSMEM
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                                                                  Science
[2]
                                                                              BONFINI L., KARLOVICH C.A., "The Son of sevenless gene Science 255:603-606(1992).
                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopteryda; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                               SEQUENCE FROM N.A. STRAIN=OREGON-R;
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Best Local
                                                         SC25_YEAST STANDARD; PRT; 1253 AA. p14771;
01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
SCD25 PROTEIN.
SCD25 OR SDC25 OR YLL016W.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi, Ascomycota; Hemiascomycetes; Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  crucial steps in sign kinase."; Cell 67:701-716(1991)
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-I- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN
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BOY-MARCOTTE E. DAMAK F., CAMONIS J., GARREAU H., JACQUET BOY-MARCOTTE E. DAMAK F., CAMONIS J., GARREAU H., JACQUET THE C-terminal part of a gene partially homologous to CDC suppresses the cdc25-5 mutation in Saccharomyces cerevisiae Gene 77:21-30(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 90260633.
CRECHET J.B., POULLET P., MISTOU M.-Y., PARMEGGIANI A., BOY-MARCOTTE E., DAMAK F., JACQUET M.;
"Enhancement of the GDP-GTP exchange of RAS proteins by terminal domain of SCD25.";
Science 248:866-868(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAMAK F., BOY-MARCOTTE E., LE ROSCOUBT D., GUILBAUD R., JA "SDC25, a CDC25-11ke gene which contains a RAS-activating is a dispensable gene of Saccharomyces cerevisiae."; mol. Cell. Biol. 11:202-212(1991).
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DAMAK F., BOY-MAR
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                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REY I., SCHWEIGHOFFER F., BARLAT I., CAMONIS J., BOY-GUILBAUD R., JACQUET M., TOCQUE B.;
"The COOH-domain of the product of the Saccharomyces gene elicits activation of p21-ras proteins in mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION.
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PFAM; PF00617; RASGEF; 1.
PFAM; PF00618; RASGEFN; 1
                                                                                                                                                                                                                                                                                                                         EMBL; M26647; AAA16565.1; PIR; S14177; S14177.
                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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                                                                                                                                                        SEQUENCE
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                           KLMDPKKNFINYRNELKSLHSAPCVPFFGVYLSDLTFTDSGNPDYL 1126
                                                  SKRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSRLALTWEKLPSKFKKFYAEFE 735
 SLMDPSRNHRAYRLTVAKLEP-PLIPFMPLLIKDMTFTHEGNKTFI
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Pred. No. 1.8
26; Mismatch
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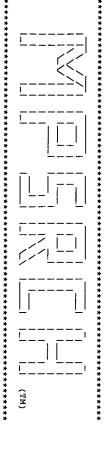
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BERGOLD P.J., BEUSHAUSEN
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15-DEC-1999 (Rel.
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regulated in aplysia sensory neurons during long-term
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCHWARTZ J.H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e by non-profit institutions as long dified and this statement is not removed. titles requires a license agreement (See send an email to license@isb-sib.ch).
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SIMILARITY: CONTAIN
SIMILARITY: BELONGS
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                                LSHLSTTYKRELAGYLIFESHAKGGTYLFNQGEEGTSWYIILKGSYNVVIYGKGVVCTLH 254
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TE; PS00888; CNMP_BINDING_1;
TE; PS00889; CNMP_BINDING_2;
TE; PS50042; CNMP_BINDING_3;
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EMBL; U39652; AAA80401
PIR; A35076; OKKW1R.
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematc
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                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Apr 22 13:18:40 2000; MasPar time 36.15 Seconds
941.038 Million cell updates/sec

Tabular output not generated.

Title: >US-09-422-999-18
Description: (1-849) from US09422999.pep
Perfect Score: 6222

Perfect Score: 6222
Sequence: 1 MYLMKRALTMTGFLTRRTHL.....VIDNQRTLSQMSHRLEPRRP 849

Scoring table: PAM 150 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir62

Statistics:

pir62
1:pir1 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 53.983; Variance 117.292; scale 0.460

SUMMARIES

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ALIGNMENTS

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KVEQYVHAGSSVVFRQGEIGVVWYIVLKGAVEVNVNGK-IVCLLREGDDFGKLALVNDLPR 646	SKSITLLSSVAPETLFLMIVSKPGFERSPEELEVVYEELTFIKALSHLSTMVKRQLSNFV 587 : : : : : : : :	SRIQMSAIWQVLLNNGLISHIDGEHQFLDKTNSYYRWVQQFRSRNKVAPSIEEV 527 :: :: : : : : :: : : : :: :: : : : : : : : : :	EKQIRDSGGILHRKMLTDNHQVIRDITTEHTRVQNCMIGAEMIDWLLTLFVSTSTTCSSL 473 : : :	Query Match 30.9%; Score 1922; DB 2; Length 1213; Best Local Similarity 38.5%; Pred. No. 0.00e+00; Matches 311; Conservative 204; Mismatches 259; Indels 33; Gaps 24;	#length 1213 #molecular-weight 139379 #checksum 3211	#domain CDC25-type quanine nucleotide exchange activator	#domain cAMP receptor protein cyclic nucleotide-binding	activator homology	<pre>/42/1; //0/3; 10/4/2; 110/3; 110/3 #superfamily cAMP receptor protein cyclic nucleotide-binding domain homology; CDC25-type quantine nucleotide exchange</pre>	196/3; 238/1; 263/3; 312/3; 444/3; 519/3; 550/2; 669/2;	**CIOSS-IEIEIEUCES EMBL:630463; NID:g4384/9; FID:g438480	1-1213 ##label SMI	##molecule_type DNA	preliminary	submitted to the EMBL Data Library, March 1994 \$42368	Smith, A.	S42368	07-Aug-1998	ame Caenorhabditis elegans	\$42368 #type complete guanine nucleotide releasing factor homolog - Caenorhabditis elegans

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RESULT
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 Query Match
Best Local Similarity
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PC1114
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SKCDC25 protein - yeast (Saccharomyces kluyveri) (fragment)
#formal_name Saccharomyces kluyveri
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
09-Sep-1997
                                                                                                                                                                                                                                                                                   Identification and analysis of a DNA fragment from Saccharomyces kluyveri that can complement the loss CDC25 function in Saccharomyces cerevisiae.
                                                                                                                                    #superfamily CDC25-type
homology
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                                                                                                                 transmembrane protein
                                                  #length
                                                              #domain CDC25-type guanine
homology #label SOS
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:es GB:M82964; NID:g171186; PID:g171187
 5.1%;
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                                    IEPKLP 1243
                                                                                                            VNFSKMRMISHIIREIRQFQQTTYKIEP-QP-KVTQYL---VDETFVLDDE-SLYEASLR 1237
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LEPRRP
                                                                          VNFEKMRMIANTARTVRYYRSQPFNPDAAQANKNHQDVRSYVRQLNVIDNQRTLSQMSHR
                                                                                                                                                    SKFKKFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFMPLLIKDMTFTHEGNKTFIDN-L
                                                                                                                                                                                                                                  VTEICLCSQ-LSKRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSRLALTWEKLP
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Similarity 26.4%;
65; Conservative
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#superfamily CDC25-type guanine nucleotide exchange activator
homology; CDC24 homology; pleckstrin repeat homology
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guanine-nucleotide-releasing protein -
CDC25 protein homolog
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Nature (1992) 358:351-354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
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#domain CDC25-type guanine nucleotide exchange activator homology #label SOS
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Pred. No. 9.95e-30;
74; Mismatches 98
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#accession B46199
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##molecule_type nucleic acid
##residues 1029-1030,'D',1032-1224 ##label WEI
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Local Similarity 23.6%;
nes 49; Conservative
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                                           VNFSKMRMISHIIREIRQFQQTTYKIDP 1227
                                                                                                                                     KQTKSLLDKLQKLVSSDGRFKNLRESLRNCDPPCVPYLGMYLTDLVFIEEGTPNYTEDGL 1199
  VNFEKMRMIANTARTVRYYRSQPFNPDA 811
                                                                                            SKFKKFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFMPLLIKDMTFTHEGNKTFIDN-L 783
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D.; Dasgupta, C.; Li, P.; Liu, B.X.; Broek, D.
Proc. Natl. Acad. Sci. U.S.A. (1992) 89:7100-7104
Identification of a mammalian gene structurally and
functionally related to the CDC25 gene of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martegani, E.; Vanoni, M.; Zippel, R.; Coccetti, P.;
Brambilla, R.; Ferrari, C.; Sturani, E.; Alberghina, L.
EMBO J. (1992) 11:2151-2157
Cloning by functional complementation of a mouse cDNA
encoding a homologue of CDC25, a Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily CDC25-type guanine nucleotide exchange activator
homology; CDC24 homology; pleckstrin repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homology #label SôS
#length 1260 #molecular-weight 143900 #checksum 9725
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#domain CDC25-type guanine nucleotide exchange activator
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Pred. No. 1.40e-26;
63; Mismatches 93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #title Identification of a human guanine nucleotide-releasing factor (H-GRF55) specific for Ras proteins. #cross-references_MVID:93275641
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                                                                                                                                1146 LKKTWLKVSKQTKALIDKLQKLVSSEGRFKNLREALKNCDPPCVPYLGMYLTDLAFIEEG 1205
                                                                                                                                                                                                                       1086 KHFNDISNLIASEIIRNEDINARVSAIEKWVAVADICRCLHNYNAVLEITSSMNRSAIFR 1145
                                                                                                                                                                               656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##cross-references GB:S62035; NID:g386046; PID:g386047
IFICATION #superfamily CDC25-type guanine nucleotide exchange activator homology; CDC24 homology; pleckstrin repeat homology
776
                                                                                           716
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##residues 787-1275 ##label RES
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NKTFIDN-LVNFEKMRMIANTARTVRYYRSQPFNPD
                                       TPNYTEDGLVNFSKMRMISHIIREIRQFQQTAYKIE 1241
                                                                                                                                                                               RRFNEIQFWVVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSR 715
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                                                                                      LALTWEKLPSKFKKFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFMPLLIKDMTFTHEG
                                                                                                                                                                                                                                                                                         4.6%;
Similarity 25.6%;
                                                                                                                                                                                                                                                                      40;
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Oncogene (1993) 8:1477-1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to GenBank, December 1994
Cloning and analysis of the full length human
ras-specific nucleotide exchange factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D.; Dasgupta, C.; Li, P.; Liu, B.x.; Broek, D. Proc. Natl. Acad. Sci. U.S.A. (1992) 89:7100-7104 Identification of a mammalian gene structurally and functionally related to the CDC25 gene of Saccharomyces
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#formal_name Homo sapiens #common_name man
19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change
10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schweighoffer, F.; Faure, M.; Fath, I.; Chevallier-Multon, M.C.; Apiou, F.; Dutrillaux, B.; Sturani, E.; Jacquet, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wei, W.; Mosteller, R.D.; Sanyal, P.; Gonzales,
                                                                                                                                                                                                                                                                                                                                                            #length 1275
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#domain CDC25-type guanine nucleotide exchange activator
homology #label SOS
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                                                                                                                                                                                                                                                                   Score 287; DB 2; Length 1275
Pred. No. 6.36e-26;
49; Mismatches 66; Indels
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                                                                                                                                                                                                                                                                                                              Length 1275;
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RESULT ENTRY

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#type complete

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Best Local
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                                                                                                                                                                                                                   #authors Bowtell, D.; Fu, P.; Simon, M.; Senior, P.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:6511-6515
#title Identification of murine homologues of the Drosophila
#title sevenless gene: potential activators of ras.
#cross-references_MUID:92335328
                                       739-982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Hughes, D.A.; Fukui, Y.; Yamamoto, M.
#journal Nature (1990) 344.355-357
#title Homologous activators of ras in fission
#cross-references MUID:90190870
#accession S28098
                                                                                                                                                                                                       #accession
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                                                                                                        ##cross-references EMBL:Z11664; NID:g54136; PID:g54137
FICATION #superfamily CDC25-type guanine nucleotide
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##cross-references EMBL:X53254; N
                                                                                                                                                ##residues
                                                                                                                                                               ##molecule_type mRNA
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Local Similarity 22.2%;
nes 57; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIISALNSSPIHRLRKTWANLNSKTLASFELLNNLTEARKNFSNYRDCLENCVLPCVPFL 814
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                                                                                                                                                                                                                                                                                                                                                $25714 #type fragment
son-of-sevenless-2 protein - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
17-Mar-1999
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#formal_name Schizosaccharomyces pombe
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
09-Sep-1997
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                 #domain pleckstrin repeat homology #label PLK\
#domain CDC25-type guanine nucleotide exchange homology #label SOS
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homology #label SOS
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                                                                                         pleckstrin repeat homology
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#checksum 7302
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Pred. No. 1.89e-24;
75; Mismatches 119
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#accession A37488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##status preliminary; not compared with conceptual translation
##molbecule_type mRNA
#residues 1-1333 ##label CHA
##residues sequence extracted from NCBI backbone (NCBIP:132148)
##note sequence extracted from nucleotide exchange activated the property of the property of
                                                                                                                764
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Local Similarity 25.4%;
hes 58; Conservative
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                                                                                                                LLIKDMTFTHEGN-KTFI--DN-LVNFEKMRMIANTARTVRYYRSQPF
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llarity 24.9%;
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#domain CDC25-type guanine nucleotide exchange
homology #label SOS
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Pred. No. 1.67e-22;
70; Mismatches 92;
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Bar-Sagi,
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                                                                                              ##molecule_type mRNA

1-1336 ##label BOW

##residues 1-1336 ##label BOW

##cross-references EMML:Z11574; NID:954134; PID:954135

##CCATION #superfamily CDC25-type guanine nucleotide of

homology; pleckstrin repeat homology
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##cross-references EMBL:M94160; NID:g170834; PID:g170835
FICATION #superfemily SH3 homology; CDC25-type guanine
exchange activator homology
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#formal_name Mus musculus #common_name house mouse
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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A Candida albicans homolog of CDC25 is functional in
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#formal_name Candida albicans
20.Feb-1995 #sequence_revision 20.Feb-1995 #text_change
09_Sep-1997
                                                                                                                                                                                                                                              Bowtell, D.; Fu, P.; Simon, M.; Senior, P.
proc. Natl. Acad. Sci. U.S.A. (1992) 89:6511-6515
Identification of murine homologues of the Drosophila
sevenless gene; potential activators of ras.
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llarity 25.48;
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1 - mouse
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#domain CDC25-type guanine nucleotide exchange activator
homology #label SOS
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#domain CDC25-type guanine nucleotide exchange activator
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Pred. No. 2.03e-20;
60; Mismatches 87;
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Best Local Similarity 25.48;
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                                                                                    RAS/adenylate cyclase pathway. #cross-references MUID:87131091
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                                                                                                                                                                                                             ##molecule_type DNA
1-496,'Y',498-953,'LSVIMNLSR',964-1589 ##label
##cross-references EMBL:X03579; NID:g3483; PID:g3484
                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type DNA
#residues 1-1589 ##label PAU
##cross-references EMBL:U17247; NID:g577216; PID:g577222; MIPS:YLR310c
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##residues 1-1589 ##label BRO
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                                 ##molecule_type DNA
##residues 877-1589 ##label DAN
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                 ##cross-references EMBL:X03579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rauley, A. submitted to the EMBL Data Library, November 1994. The sequence of S. cerevisiae cosmid L2142. $51442
                                                                                                                                                                                                                                                                                                                                                               Camonis, J.H.; Kalekine, M.;
Boy-Marcotte, E.; Jacquet,
EMBO J. (1986) 5:375-380
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The S. cerevisiae CDC25 gene product regulates
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31-Mar-1988 #sequence_revision 31-Mar-1993
26-Feb-1999
                                                                                                                                                                                                                                                                                                                                Characterization, cloning and sequence analysis of the CDC25 gene which controls the cyclic AMP level of Saccharomyces
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                                                                         S43051
                                                                                                                                                                               Daniel, J.H.
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11 (1987) 48:789-799
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Pred. No. 9.72e-21;
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Best Local Similarity 25.5%;
Matches 71; Conservative
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1301-1542
Query Match
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                                                                                                                                                                                                                                              ##molecule_type mRNA
                                                                                                                                       ElyBase:Sos
#arross-references FlyBase:FBgn0001965
FICATION #superfamily CDC25-type guanine nucleotide exchange
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                                                                                                                                                                                                                                                                                                               Rasl and a putative guanine nucleotide exchange factor perform crucial steps in signaling by the sevenless tyrosine kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           guanine nucleotide exchange activator son-of-sevenless
  fruit fly (Drosophila melanogaster)
#formal_name Drosophila melanogaster
28-May-1992 #sequence_revision 28-May-1992 #text_change
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Cell (1991) 67:701-716
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                                 #length
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                                                                                                                        homology; pleckstrin repeat homology
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#domain CDC25-type guanine nucleotide exchange activator
homology #label SOS
                                              #domain pleckstrin repeat homology #label PLK\
#domain CDC25-type guanine nucleotide exchange activator
homology #label SOS
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SGD:S0004301; MIPS:YLR310c
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                                 #molecular-weight 177933 #checksum
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 Score 251;
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NID:g158470;
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Matches 48; Conservative
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NCE $64761
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##cross-references EMBL:Z73121; NID:gl360186;
MIPS:YLL016w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##experimental_source strain S288C
NCE S69380
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                                                                                                                                                                                                                                                                                            ##residues 1-1048 ##label PUR ##cross-references EMBL:X97560; NID:91297003; PID:e238680; PID:91297014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##cross-references EMBL:273121; NID:g1360186;
MIPS:YLL016w
            ##cross-references EMBL:X91488; NID:g1495203; PID:e199006;
                                   ##residues
                                                  ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENYEERLAIMQRAIEVMMVMLELNNFNGILSIVAAMGTASVYRLRWTFQGLPERYRKFLE 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECRELSD-DHLKK-YQERLRSINPPCVPFFGRYLTNILHLEEGNPDLLANTELINFSKRR 1009
                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, April 1996
The sequence of 32 kb on the left arm of yeast chromosome Xi
reveals 14 open reading frames among which HSP104, SSA2,
SPA2, KNS1, DPS1/APS, SDC25, a new member of the
seripauperins family and a new ABC transporter homologous
to the human multidrug resistance protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCD25 protein (version 2) - yeast (Saccharo protein L1309; protein YLLO16w #formal_name Saccharomyces cerevisiae 01-aug-1995 #sequence_revision 24-May-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goffeau, A.; Purnelle, B. submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             $64758; $64764; $69390; $70559
$64743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the Protein S64758
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                                                                                                                                                  Sequence analysis of the CEN12 region of Saccharomyces cerevisiae on a 43.7 kb fragment of chromosome XII including an open reading frame homologous to the human cystic fibrosis transmembrane conductance regulator protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S64764
                                                                                                                                                                                                                                   Miosga, T.; Zimmermann, F.K.
Yeast (1996) 12:693-708
                                                                                                                                                                                                                                                                                                                                                          S69390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purnelle, B.; Goffeau, A.
                                                                                                S70559
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the nucleotide sequence was
                                                                         nucleic acid sequence not shown;
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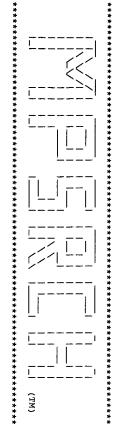
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#map_position 12L
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#accession S12942
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                                                                                                                                                                                                                                                                                                                                           ##residues 1-737,'A',738-970,'I',972-1250 ##label DAM2
##cross-references EMBL:M26647
##note the authors translated the codon GAG for residue 538 as
##note Asp, GTC for residue 550 as Asp, and CTA for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      816 SKRAKLLSHFIFIAEYCRKFNNFSSMTAIISALYSSPIYRLEKTWQAVIPQTRDLLQSLN 875
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                    ##cross-references SGD:S0003939; MIPS:YLL016w
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Similarity 34.0%;
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Mol. Cell. Biol. (1991) 11:202-212
SDC25, a CDC25-like gene, which contains a RAS-activating domain and is a dispensable gene of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               $14177 #type complete
$CD25 protein (version 1) - yeast (Sac
protein 11309; protein YLD016w
#formal_name_Saccharomyces_cerevisiae
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                                                                                                                                                                                                           The C-terminal part of a gene partially homologous to CDC25 gene suppresses the cdc25-5 mutation in Saccharomyces
                                                                                                                                                                                                                                                                   Boy-Marcotte, E.; Damak, Jacquet, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, August 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S14177; S12942; PS0040
S14177
                                     SGD:SCD25; SDC25
                                                                                                                                                                                                                                                      Gene (1989) 77:21-30
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                                                                          668-679, 'NPVMTILMC', 689,'N', 691-1250 the authors translated the codon GCA Asp and GAT for residue 748 as Ala
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804 as Lys
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Pred. No. 2.32e-18;
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                                                                                                                                                                                                                                                                                         F.; Camonis, J.; Garreau,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##cross-references EMBL:X62382; NID:g5587; PID:g5588
##note this protein is identified as the N4 isoform
#The inactive form of the enzyme is composed of two regulatory
chains and two catalytic chains. Activation by cAMP produces two
active catalytic monomers and a regulatory dimer that binds four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 736 SLMDPSRNHRAYRLTVAKLEP-PLIPFMPLLIKDMTFTHEGNKTFI 780
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Similarity 33.0%;
35; Conservative
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Neuron (1992) 8:387-397
A regulatory subunit of the cAMP-dependent protein kinase down-regulated in aplysia sensory neurons during long-term sensitization.
form) #status predicted\
#binding_site cAMP (Glu, Arg) #status predicted\
#binding_site cAMP (Glu, Arg) #status predicted
#binding_site cAMP (Glu, Arg) #status predicted
#length 378 #molecular-weight 42737 #checksum 2977
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protein kinase (EC 2.7.1.37), cAMP-dependent, type I
regulatory chain - California sea hare
#formal_name Aplysia californica #common_name California sea
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                                                                                                                                                                                                                                                                                                                                                                         acetylated amino end; ATP binding; cAMP binding; duplication;
heterotetramer; homodimer; phosphoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #length 1250 #molecular-weight 144779 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                    #superfamily cAMP-dependent protein kinase regulatory chain; cAMP receptor protein cyclic nucleotide-binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JH0590
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                                                                                                                                                                       #product protein kinase, cAMP-dependent, type I-beta
regulatory chain *status predicted *label MAT\
#domain protein interaction *label DIM\
#region pseudophosphorylation motif\
#domain cAMP receptor protein cyclic nucleotide-binding
domain homology *label CAI\
                                                                                              #domain cAMP receptor protein cyclic nucleotide-binding domain homology #label CA2\
#modified_site acetylated amino end (Ala) (in mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-378 ##label BER
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Pred. No. 9.82e-18;
26; Mismatches 44
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Db
Search completed: Sat Apr 22 13:19:19 2000 Job time : 39 secs.
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3.5%; Score 216; DB 1; Length 378;
Best Local Similarity 32.7%; Pred. No. 1.21e-14;
Matches 33; Conservative 26; Mismatches 39; Indels 3; Gaps
                                                                                                                                                 193 EGGSFGELALIYGTPRAATVKAKTDV-KLWGIDRDSYRRIL 232
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255 EGDDFGKLALVNDAPRAASIVLREDNCHFLRVDKEDFNRIL 295
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Apr 22 13:23:13 2000; MasPar time 14.86 Seconds 759.883 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: >US-09-422-999-18 (1-849) from US09422999.pep 6222

Sequence: 1 MYLWKRALTMTGFLTRRTHL.....VIDNQRTLSQMSHRLEPRRP 849

Scoring table: PAM 150 Gap 11

Searched: 134018 seqs, 13297625 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT9_COMB 5:backfiles1

Statistics: Mean 36.052; Variance 179.682; scale 0.201

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
287 287 287 276 276 266 255 255 255 255 251 143 1143 1143 1133 1133 1133	Score
44444666000000000000000000000000000000	Query Match
489 666 814 402 623 1297 1319 1336 426 1336 1372 1372 1372 1372 1572 852 852 852 768 852 758	Length
1110100100000000000000	DB
US-08-318- US-08-318- US-08-290- US-08-363- US-08-363- US-08-363-	ID
Sequence 4, Applicatio Sequence 2, Applicatio Sequence 2, Applicatio Sequence 14, Applicatio Sequence 11, Applicatio Sequence 11, Applicatio Sequence 11, Applicatio Sequence 10, Applicatio Sequence 10, Applicatio Sequence 10, Applicatio Sequence 2, Applicatio Sequence 5, Applicatio Sequence 5, Applicatio Sequence 13, Applicatio Sequence 13, Applicatio Sequence 5, Applicatio Sequence 5, Applicatio Sequence 5, Applicatio Sequence 2, Applicatio Sequence 3, Applicatio Sequence 14, Applicatio Sequence 14, Applicatio Sequence 3, Applicatio Sequence 3, Applicatio Sequence 14, Applicatio Sequence 3, Applicatio Sequence 3, Applicatio Sequence 3, Applicatio	Description
1. 23e-12 1. 23e-12 1. 23e-12 1. 23e-12 1. 23e-12 1. 3e-12 1. 5. 22e-11 1. 5. 22e-11 1. 6. 3.07e-10 1. 3.67e-10 1. 3.67e-02 1. 3.67e-02 1. 3.67e-02 1. 3.67e-02 1. 3.67e-02 1. 3.67e-02 1. 3.67e-00 1. 3.67e-00 1. 6.37e-02 1. 6.37e-02 1. 6.37e-02 1. 6.37e-02 1. 6.37e-02 1. 6.37e-02 1. 6.37e-02 1. 6.37e-02 1. 6.37e-02 1. 6.37e-02	Pred. No.

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Applicatio	Applicati	Applicatio	Applicatio	Applicati	Applicati	Applicatio	Applicatio	Applicati	Applicatio	Applicatio	Applicatio	Applicatio	コプアナナイグイン								
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TELEFAX: (610) 454-3808 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 489 amino acids	TELECOMMUNICATION INFORMATION: TELEPHONE: (610) 454-3839	REFERENCE/DOCKET NUMBER: ST92033-US	Julie K.	Y/AGENT I	~	APPLICATION NUMBER: FR92/04827	CEASSIFICATION: 435	9	APPLICATION NUMBER: US/08/318,831	LICATION DATA:	Word 5.1	OPERATING SYSTEM: System 7.1	COMDITARD: Macintock	COMPUTER READABLE FORM:	19426	F	STATE: PA	a	00 Arcola Road, 3C43	ADDRESSEE: Rhone-Poulenc Rorer Inc.	DENCE ADDRESS	R OF SEQUENCES:	OF INVENTION: PREPARATION AND UTILIZATION	OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCE	NVENTION:	Tocque, Bruno	APPLICANT: Schweighoffer Fabien	z		Sequence 4, Application US/08318831		Sequence 4, Application US/08318831			XXXXXX	Direction of the second	IIC-08-318-831-4 STANDARD. DRM. 489 AA

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Best Local Similarity 25.6%;
Matches 40; Conservative
                         SEQUENCE
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                                                                 TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                             REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST920
TELECOMMUNICATION INFORMATION:
                                                                                                                                                 APPLICATION NUMBER: FR92, FILING DATE: 21-APR-1992 ATTORNEY/AGENT INFORMATION: NAME: Smith Julie K.
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tocque, Bruno
TITLE OF INVENTION: PEPT:
TITLE OF INVENTION: ACTIV
TITLE OF INVENTION: PREPA
                                                                                                                                                                                               CLASSIFICATION: 435 PRIOR APPLICATION DATA:
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                                              TYPE:
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                       TOPOLOGY: 1:
CE 666 AA;
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489 AA; 55488 MW;
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                                                         666 amino acids
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0 Arcola Road, 3C43
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                                                                                                      (610) 454-3839
                       75236 MW; 2256870 CN;
                                                                                                                                                                                                                      19 October 1994
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ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SAID PEPTIDES
PREPARATION AND UTILIZATION
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 Score 287;
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Pred. No. 1.23e-12;
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625 KHENDISNLIASEIIRNEDINARVSAIEKWVAVADICRCLHNYNAVLEITSSMNRSAIFR 684
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                                                                                                                                               TELEFAX: (610) 454-3808 INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
                                                                                                                                                                                                                  FILING DATE: 21-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie K.
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APPLICATION NUMBER: I
                                                                                                                                                                                                                                                                                                                SOFTWARE: Word 5.1 (EPO Patentin)
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
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                                                                                                 LENGTH: b14 ...

TYPE: amino acid

Tinear
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                                                                                                                                                                                                        NAME: Smith, Julie I REGISTRATION NUMBER:
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CE 814 AA; 91292 MW; 3388819 CN;
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500 Arcola Road, 3C43
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ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SAID PEPTID
PREPARATION AND UTILIZATION
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                                    Score 287; DB 1; Le
Pred. No. 1.23e-12;
49; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.23e-12; 49; Mismatches 66;
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                                                           Length 814;
                                      Indels
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Query Match
Best Local :
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                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08290731C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              745 TPNYTEDGLVNFSKMRMISHIIREIRQFQQTAYKIE 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   716 LALTWEKLPSKFKKFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFMPLLIKDMTETHEG
584 EQFDSLTPLPEQEGPTVGTVGTVFELMSSKDLAYQMTIYDWELFNCVHELELIYHTFGRHN 643
                146 QELEDLS-LHNSPDPIIYKDELVLLLPPRETAKQLCILEFQSFSHISRIQFLTKIWDELN 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08290731C Patent No. 5843646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                             TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
                                    Local Similarity es 57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ITTLE OF INVENTION: STITLE OF INVENTION: A NUMBER OF SEQUENCES:
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PL0921/92
FILING DATE: 17-FEB-1992
                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU93/00068
FILING DATE: 17-FEB-1993
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPA
OPERATING SYSTEM: PC-DO
SOFTWARE: PATENTIN Rela
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                            REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: Q-36066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
                                                                                                                                                                                                      FILING DATE: 17-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: KIT, GORDON
                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKKTWLKVSKQTKALIDKLQKLVSSEGRFKNLREALKNCDPPCVPYLGMYLTDLAFIEEG
                                                                                           TYPE: ami
                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
ZIP: 20
                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/290,731C FILING DATE: 17-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & STREET: 2100 PENNSYLVANIA AVENUE, N.W.
                                                                         LE TYPE: protein
402 AA; 47252 MW; 844812 CN;
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                                                                                                     i: 402 amino acids
amino acid
                                   4.4%;
llarity 22.2%;
Conservative
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VENTION: DNA MOLECULES ENCODING MURINE
VENTION: SON OF SEVENLESS (mSOS) GENE,
                                                                                                                                                                                                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                      Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                           15
                                   Score 276; DB 2; Lo
Pred. No. 8.79e-12;
75; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                     Length 402
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                                    Indels
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                                   Gaps
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                                             SEQUENCE
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Query Match 4.4%;
Best Local Similarity 25.8%;
Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383 ISRERNTNNI-YQRSLT 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08318831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     703 AIVMGLSNIAVSRLALTWEKLPSKFKKFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19426
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: Macintosh
COMPUTER: Floppy
COMPUTER: US/08/318,
FILING DATE: 19 October 1994
CLASSIFICATION: 435
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                                                                                                                                                           TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: F892/04827
FILING DATE: 21-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie K.
REGISTRATION NUMBER: P-38,619
REGISTRATION NUMBER: P-38,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tocque, Bruno
TITLE OF INVENTION: PETTIDES HAVING A GDP EXCHANGE FACTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SAID PETTID
TITLE OF INVENTION: PREPARATION AND UTILIZATION
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 500 ALCOLUCITY: Collegeville
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                                                                                              652 AA; 74235 MW; 2320730 CN;
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00 Arcola Road, 3C43
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Score 276; DB 1; Le
Pred. No. 8.79e-12;
71; Mismatches 89;
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                                              Length 652;
  Indels 10;
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Query Match
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REFERENCE/DOCKET NUMBER: Q-36
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELERAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-290-731C-11
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APPLICANT: BOWTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIF CHARLES PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU93/00068
TITING DATE: 17-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 17-FEB-1992
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                  TYPE: ami
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SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 2100 FEM.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PL09 FILING DATE: 17-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 17-OCT-1994
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                                                                                                                                                                                                                                              ENGTH:
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                                                                                                                                                                                                      amino acid
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                                                                            XPE: protein
AA; 49877 MW; 918596 CN;
                                                                                                                                                                                                                                                   423 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
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4.3%;
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Score 266;
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Length 423;
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Matches 57; Conservative
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                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: Patentin Release #1.0, Ve CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,731C FILING DATE: 17-OCT-1994 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    763 PLLIKDMTFTHEGNKTFI---D-NLVNFEKMRMIANTARTVRYYRSQPF 807
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                                                               TELEFAX: (202) 293-78
TELEX: 6491103
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                           APPLICATION NUMBER: PL0921/92
FILING DATE: 17-FEB-1992
ATTORNEY_RGENT INFORMATION:
NAME: KIT, GOIDON
                                                                                                                                                                                                              APPLICATION NUMBER: PCT/AU93/00068 FILING DATE: 17-FEB-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                  REFERENCE/DOCKET NUMBER: Q-
TELECOMMUNICATION INFORMATION:
                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1297 amino aci
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CORRESPONDENCE ADDRESS:
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               TOPOLOGY:
                         TYPE: amino acid
                                                                                                       TELEPHONE:
                                                                                                                                              REGISTRATION NUMBER:
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                                       1297 amino acids
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                                                                                           (202) 293-70
(202) 293-7860
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protein
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                                                                                                          293-7060
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                                            TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 4.3%;
Local Similarity 24.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                   APPLICATION NUMBER: FR92, FILING DATE: 21-APR-1992
ATTORNEY/AGENT INFORMATION: NAME: Smith, Julie K.
REGISTRATION NUMBER: P-38
                                                                                                                                                                                                                                 COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (EPO Pate)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: TOCQUE, Bruno TITLE OF INVENTION: PEPTI TITLE OF INVENTION: ACTIV TITLE OF INVENTION: PREPA
                                                                                              REFERENCE/DOCKET NUMBER: ST
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIYLTNILKTEEGNSDFLKRKGKDLINFSKRRKVAEITGEIQQYQNQPY 942
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                                                                                                                                                                                                                                                                                                                      STATE:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                               STREET:
                     TYPE: amino acid
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            TOPOLOGY:
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364 AA; 41968 MW; 717826
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500 Arcola Road, 3C43
                                    364 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                        PEPTIDES HAVING A GDP EXCHANGE FACTOR ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SAID PEPTIDES PREPARATION AND UTILIZATION
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                                                                                                                                                                                                                                              (EPO Patentin)
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                                                                                                           P-38,619
ER: ST92033-US
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Pred. No. 5.22e-11;
70; Mismatches 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
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Query Match
Best Local Similarity
Matches 58; Conser
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                                                TELEFAX: (202) 293-784
TELEX: 6491103
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
                             SEQUENCE CHARACTERISTICS:
                                                                                                               REFERENCE/DOCKET NUMBER: Q-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                             APPLICATION NUMBER: PL09
FILING DATE: 17-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  FILING DATE: 17-FEB-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVMGLSNIAVSRLALTWEKLPSKFKKFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFMP
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                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                    FILING DATE: 17 CLASSIFICATION:
                                                                                               TELEPHONE:
                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/AU93/00068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: WASHINGTON
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               LENGTH:
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NO. 5843646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         20037
: 423 amino acids amino acid
                                                                                                                                                                   KIT, Gordon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOWTELL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUGHRUE,
                                                                                                   (202)
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25.48;
                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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                                                                                                                                                                                                                                                   17-FEB-1993
                                                                                   293-7860
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                                                                                                   293-7060
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Pred. No. 3.07e-10;
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Best Local :
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Local Similarity 25.4%;
Nes 58; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PL0921/92
PTITING DATE: 17-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BOWTELL, David Douglas Lawrence TITLE OF INVENTION: DNA MOLECULES ENCODING I TITLE OF INVENTION: SON OF SEVENLESS (MSOS) TITLE OF INVENTION: AND mSOS POLYPEPTIDES
                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                               TELECOMMUNICATION INFORMATION:
                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                 STREET: 210,
CTTY: WASHINGTON
                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                    REGISTRATION NUMBER: 30,764
                                                                                                                                              APPLICATION NUMBER: PCT//
FILING DATE: 17-FEB-1993
                                                                                                                                                                                            APPLICATION NUMBER: US/08/290,731C FILING DATE: 17-OCT-1994
                         TELEFAX:
                                   TELEPHONE:
                                                              REFERENCE/DOCKET NUMBER:
                                                                                      NAME:
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                                                                                KIT, Gordon
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               6491103
                         E: (202) 293-70
(202) 293-7860
                                                                                                                                                                                                                                                                                                     USA
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  ID NO:
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                                     293-7060
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Pred. No. 3.67e-10;
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08290731C Patent No. 5843646
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                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                           APPLICATION NUMBER: US/08/
FILING DATE: 17-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU
FILING DATE: 17-FEB-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        GENERAL
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                                                                                                                   OPERATION SYSTEM: PC-DOS/MS-VO
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
US/08/290,731C
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
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LENGTH: 426 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                  STATE: I
COUNTRY:
ZIP: 200
                       APPLICATION NUMBER: PL09 FILING DATE: 17-FEB-1992
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Similarity 25.5%;
71; Conservati
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                                                                                                                                                   PatentIn Release #1.0, Version #1
Gordon
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                                                                                                                                                                                                                                                                                                                    David Douglas Lawrence
DNA MOLECULES ENCODING
SON OF SEVENLESS (mSOS)
AND mSOS POLYPEPTIDES
                                                                          PCT/AU93/00068
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                                     PL0921/92
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Pred. No. 3.67e-10,
77; Mismatches 11
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REGISTRATION NUMBER:

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TELEFAX: (202) 293-7860
TELEFAX: (491103
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                            APPLICANT: BOWTELL, Dav
TITLE OF INVENTION: DNA
TITLE OF INVENTION: SON
TITLE OF INVENTION: AND
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 1319 AA; 150882 MW;
                             CURRENT APPLICATION NUMBER: US/08/290,/31C APPLICATION NUMBER: US/08/290,/31C FILING DATE: 17-OCT-1994 CLASSIFICATION: 435 CLASSIFICATION DATA: PRIOR APPLICATION DATA: PCT/AU93/00068
 APPLICATION NUMBER: PCT//
FILING DATE: 17-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PL092
                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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LENGTH: 1319 amino aci
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                                                                                                                                                                                               STREET: 2100
CTTY: WASHINGTON
                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                     USA
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15
                                                                                                                                                                                                                                                                                 David Douglas Lawrence
DNA MOLECULES ENCODING MURINE
SON OF SEVENLESS (mSOS) GENE,
                                                                                                                                                                                                                                                                                                                                                us/08290731c
                                                                                                                                                                                                                                   MION,
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Pred. No. 3.
64; Mismatc
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3.67e-10;
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                                                                                                                                                                                                                                                                            Patent No.
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                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 17-OCT-1994
                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein JENCE 1336 AA; 152734 MW; 9610574 CN;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                      STATE: D
COUNTRY:
                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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CITY: WASHINGTON
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                                                                                                                                                                                                                                            David Douglas
  PCT/AU93/00068
                                              US/08/290,731C
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Pred. No. 3.67e-10
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5843646
GENERAL INFORMATION:
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TELEX: 6491103
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF INVENTION: INVE
                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                          COMPUTER READABLE FORM:
MEDLIM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 430 amino acid
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                                                                                                                                                                                                                                                            STREET: 2100 PENICITY: WASHINGTON
  APPLICATION NUMBER: US/0 FILING DATE: 17-OCT-1994
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                                                                                                                                                                                                                  COUNTRY:
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430 AA; 50634 MW; 939381 CN;
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                                                                                                                                                                                                                                                                                       2100 PENNSYLVANIA
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JENTION: DNA MOLECULES ENCODING I
SENTION: SON OF SEVERLESS (MSOS)
JENTION: AND MSOS POLYPEPTIDES
                                                                                                                                                                                                                                                                                                               SUGHRUE,
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Pred. No. 7.43e-10;
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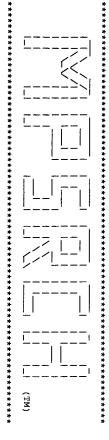
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Best Local
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                                                                                                                                                                                                                                                                                                           XXXXXX
                                                                                                                                                                                                                                                          Sequence 13, Application US/08290731C
                                                                                                                                                                                                                                                                                                                                                                                                    1010 KVAEIIGEIQQYQNQPY 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                       Sequence 13, Application Patent No. 5843646
                                                                                                                                                                                                                                                                                                                                                                                                                               733
                                                                                                                                                                                                                                                                                                                                                                                                                                                     952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     892
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                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 293-786
TELEX: 6491103
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                         APPLICANT: BOWTELL,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: Q-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: KIT, Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PL092
FILING DATE: 17-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU93/00068
FILING DATE: 17-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQLSKRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSRLALTWEKLPSKFKKFYA 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENYEERLAIMQRAIEVMMVMLELNNFNGILSIVAAMGTASVYRLRWTFQGLPERYRKFLE 951
                                                                                                                                                                                                                                                                                                                                                                                                                             EFESLMDPSRNHRAYRLTVAKLEPPLIPFMPLLIKDMTFTHEGNKTFIDN--LVNFEKMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECRELSD-DHLKK-YQERLRSINPPCVPFFGRYLTNILHLEEGNPDLLANTELINFSKRR 1009
 COMPUTER:
OPERATING
SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: ami
                                                            ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & STREET: 2100 PENNSYLVANIA AVENUE, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USA ZIP: 20037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 30,764
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1572 AA; 174116 MW;
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                               807
                                                                                                                                                         David Douglas Lawrence
DNA MOLECULES ENCODING I
SON OF SEVENLESS (mSOS)
AND mSOS POLYPEPTIDES
                                                                                                                                                                                                                                  US/08290731C
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Pred. No. 7.43e-10
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 Version #1.25
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CC CURRENT APPLICATION NUMBER: US/OB/290,731C
CC APPLICATION NUMBER: US/OB/290,731C
CC CLASSIFICATION: 435
CC CLASSIFICATION UNDER: PCT/AU93/00068
CC PRIOR APPLICATION UNDER: 0-36066
CC REFERENCE/DOCKET NUMBER: 0-36066
CC REFERENCE/DOCKET NUMBER: 0-36066
CC REFERENCE/DOCKET NUMBER: 0-36066
CC REFERENCE/DOCKET NUMBER: 0-36066
CC TELECOMMUNICATION REGRATION:
CC SEQUENCE (202) 293-7060
CC TELECHA (402) 293-7060
CC TYPE: anino acids
CC TYPE: Anino
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Sat Apr 22 13:17:33 2000; MasPar time 44.93 Seconds 447.554 Million cell updates/sec

Title:

Description: Perfect Score:

Sequence: >US-09-422-999-18 (1-849) from US09422999.pep 6222 1 MYLMKRALIMTGFLIRRTHL.....VIDNQRTLSQMSHRLEPRRP 849

Scoring table: PAM 150 Gap 11

188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq36 1:geneseqp

Statistics: Mean 38.706; Variance 183.913; scale 0.210

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 3 3 4 4 4 7 6 6 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
370 287 287 287 286 266 256 255 255 257 201 110 111 111 111 111 111 111 111	Score
	Query Match 1
1077 489 666 814 814 813 1297 1297 1336 609 933 768 933 768 528 528 528 528 528 528	Length
	DB B
R91597 R50991 R50991 R43578 R43580 R43579 R447048 R84639 R44579 R84638 R84638 R84638 W54350 W85039 W	ID
C3G protein. Peptide which modulate Mammalian son of seven mSOS2 protein. Peptide which modulate Mammalian son of seven Mammalian son of seven Mammalian son of seven MSOS1 protein. PRO-green fluorescent protein. An unann MCG7 protein. An unann MCG7 protein. PRG-green fluorescent protein fluorescent protein. PRG-green fluorescent protein separate Mycobacterium bovis paramycobacterium bovis po Virulence-associated separate Mycobacterium bovis vi Sorting nexin 2. Rat GMEB-2' protein segant	Description
1.53e-19 9.88e-13 9.88e-13 9.88e-13 7.60e-12 1.00e-10 3.02e-10 3.63e-10 3.63e-10 3.63e-10 3.19e-00 4.81e-01 4.81e-01 5.14e-01 5.17e+00 3.17e+00	Pred. No.

RESULT

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W84560	W81839	R57283	W94459	W94458	W81512	W44135	W53485	W16326	W10653	W31504	R30477	W97809	R77249	W79140	W43421	R26181	W23969	W01113	W55710	W55252
	Human LFA-1 alpha chai	Bovine enterokinase	Human neurofibromatosi	Human neurofibromatosi	Drosophila fat facets	Mus musculus factor VI	Murine factor VIII.	Nematocidal toxin 167P	Bacillus thuringiensis	Nematode toxin 167P pr	Human leukocyteHGF.	Human GTPase regulator	Babesia merozoite p58.	Plant acetolactate syn	Rat syntaxin 3 protein	TSG-14.	Connexin protein Cx43.	RNA polymerase primary	H. pylori ORF 06ep1061	H. pylori ORF 05ep1171
1.49e+02	1.49e+02	1.456+02	1.49e+02	1.49e+02	8.47e+01	1.13e+02	1.13e+02	6.35e+01	6.35e+01	6.35e+01	1.30e+02	9.77e+01	9.77e+01	6.35e+01	1.30e+02	1.13e+02	4.75e+01	4.75e+01	5.49e+01	1.45e+01

ALIGNMENTS

OV O	RES ID AC DT
Ma t	RESULT 1 ID R91597 standard; Protein; 1077 AA. RP91597; DT 26-JUL-1996 (first entry) DE C3G protein.

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Best Local S
Matches 4
                                                                                               New peptide(s) modulating GDP exchange in complexes - with ras protein and derived antibodies, nucleic acid etc. esp. for diagnosis and treatment of cancer claim 2; Page 23-24; 46pp; French.

The peptide antagonises the interaction of GDP-exchange factor with the p21-GDP complex and thereby regulates the activity of spene products. It can also be used to identify other compounds which can modulate GDP exchange. The coding sequence can be use the coding sequence can be used to interactive the coding sequence.
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                                                                                                                                                                                                                                                                                                                              N-PSDB; Q51233.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 28-OCT-1993.
19-APR-1993; F00382.
21-APR-1992; FR-004827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDP; exchange; GRF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R50990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide(s) modulating GDP exchange i protein and derived antibodies, nucleic diagnosis and treatment of cancer Claim 2; Page 25-26; 46pp; French.
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                                                  produce antisense products d for use in diagnosis e.g.
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                                                                                                                                                                                                                                                                                                                                                     93-351724/44.
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                                                     e.g. detecting
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Pred.
                                                                                 which can
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No. 9.88e-13;
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                                                  inhibit oncogene expression (over)expression of GRF for
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diagnosis;
                                                                                                        be used
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                                                                                                                                                             (GRF)
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Matches 4
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Best Local
                             Peptide which modulates GDP; exchange; GRF; GDP detection; cancer; ras;
                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis and treatment of cancer Claim 2; Page 20-22; 46pp; French.
The peptide antagonises the interaction of GDP-exchange fact with the p21-GDP complex and thereby regulates the activity gene products. It can also be used to identify other compour which can modulate GDP exchange. The coding sequence can be to produce antisense products which can inhibit oncogene expands of use in diagnosis e.g. detecting (over)expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RHON) RHONE POULENC RORER Schweighoffer F, Tocque B; WPI; 93-351724/44.
                                                                        R43580;
11-MAY-1994
 Homo sapiens.
W09321314-A.
                                                                                                     R43580 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                   typing of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptide(s) modulating GDP exchange in complexes - with protein and derived antibodies, nucleic acid etc. esp. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; Q51233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-APR-1993; F00382
21-APR-1992; FR-0048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9321314-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDP; exchange; GRF; GDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide which modulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R43578 standard;
                                                                                                                                                                776 NKTFIDN-LVNFEKMRMIANTARTVRYYRSQPFNPD
                                                                                                                                                                                                                                                                                   656 RRFNEIQFWVVTEICLCSQLSKRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSR 715
                                                                                                                                                                                                                                                                                                               625 KHFNDISNLIASEIIRNEDINARVSAIEKWVAVADICRCLHNYNAVLEITSSMNRSAIFR 684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 25.6%; nes 40; Conservative
                                                                                                                                                                                LALTWEKLPSKFKKFYAEFESLMDPSRNHRAYRLTVAKLEPPLIPFMPLLIKDMTFTHEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NKTFIDN-LVNFEKMRMIANTARTVRYYRSQPFNPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKKTWLKVSKQTKALIDKLQKLVSSEGRFKNLREALKNCDPPCVPYLGMYLTDLAFIEEG
                                                                                                                                                                                                                                                    LKKTWLKVSKQTKALIDKLQKLVSSEGRFKNLREALKNCDPPCVPYLGMYLTDLAFIEEG
                                                                                                                                                                                                                                                                                                                                            Similarity 40; Conser
                                                                                                                                                                                                                                                                                                                                                                                                      814 AA;
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                     Protein;
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                                                          GDP exchange in the p21-GDP
                                           exchange
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exchange
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDP exchange
                                                                                                       652
                                                                                                                                                                                                                                                                                                                                          Score 287; |
Pred. No. 9.1
49; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 287; DB 1;
Pred. No. 9.88e-13;
49; Mismatches 66
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factor;
                                            factor;
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                                                                                                                                                                                                                                                                                                                                                                                                                              The coding sequence can be used ch can inhibit oncogene expression ecting (over)expression of GRF for
                                                                                                                                                                                                                                                                                                                                                          DB 1;
.88e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the p21-GDP; antisense;
                                            antisense;
                                                                                                                                                                810
                                                                                                                                                                                             780
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Best Local
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19-APR-1993;
21-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis and treatment of cancer Claim 2; Page 32-34; 46pp; French.
The peptide antagonises the interaction of GDP-exchange factor (GRF with the p21-GDP complex and thereby regulates the activity of ras gene products. It can also be used to identify other compounds which can modulate GDP exchange. The coding sequence can be used to produce antisense products which can inhibit oncogene expression and for use in diagnosis e.g. detecting (over)expression of GRF for the contract of the contra
                                                                                                                                                                 The mammalian son of sevenless gene has been found to have homology with various guanine exchange factors, suggesting a possible role in protein tyrosine kinase pathways via the Ras proteins. Mutations in the genes and consequently their products may result in specific defects or tumour formation. Antagonists to the protein/gene may used to treat conditions arising from mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding mammalian son of seven-less gene and proteins encoded by it - regulates tyrosine kinase signalling pathway ras proteins, may be used for diagnosis and therapy of genetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FLOR-) FLOREY INST
Bowtell DDL;
WPI; 93-272883/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 6
R47048
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Sequence 652 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (RHON) RHONE POULENC ROI
Schweighoffer F, Tocque
WPI; 93-351724/44.
                                                                                                                                                                                                                                                                                                                                                                                                              ras proteins, may defects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R47048;
26-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide(s) modulating GDP exchange in complexes protein and derived antibodies, nucleic acid etc. es
                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Figure 2; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; Q58624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
W09316179-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tyrosine kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Son of sevenless
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalian son
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; Q51235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169
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y Match 4.3%;
Local Similarity 24.9%;
hes 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLLIKDMTFTHEGNKTFI---D-NLVNFEKMRMIANTARTVRYYRSQPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIYLTNILKTEEGNNDFLKKKGKDLINFSKRRKVAEITGEIQQYQNQPY
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                                                                                                                                       1297
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llarity 25.8%;
Conservative
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que B;
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Pred. No. 7.
71; Mismatc
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; Sos; guanine exchanç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SA
Score 266; DB 1;
Pred. No. 4.81e-11;
70; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
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.60e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exchange factor;
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                                                                   Length 1297;
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Best Local
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14-JAN-1994; 113494.
14-JAN-1994; CA-113494
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mSOS2; SOS2; (
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25-FEB-1996
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WPI; 95-302931/40.
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                                                IVMGLSNIAVSRLALTWEKLPSKFKKFYAEFESLMDPSRNH-RAYRLTVAKLEPPLIPFM
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                                                                                                                                                                                                                                                                                                                h 4.2%;
Similarity 24.9%;
57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        acute myelogenous or acute lymphocytic 1297 AA;
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1164 ...
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Pred.
70; M
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                                                                                                                                                                                                                                                                                                                   Mismatches
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No. 1.00e-10;
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763

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IRESULATED ACCOMMENTATION ACCOMMENTA
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21-APR-1992; FR-004827.
(RHON ) RHONE POULENC RORE
Schweighoffer F, Tocque E
WPI; 93-351724/44.
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R43579;
R43579;
11-MAY-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; Q51234.

New peptide(s) modulating GDP exchange in complexes - protein and derived antibodies, nucleic acid etc. esp. diagnosis and treatment of cancer Claim 2; Page 28-29; 45pp; French.
                           DNA encoding mammalian son of seven-less gene and proteins encoded by it - regulates tyrosine kinase signalling pathway via ras proteins, may be used for diagnosis and therapy of genetic
                                                                                                                                                                      (FLOR-) FLOREY INST EXPERIMENTAL BOWTE11 DDL; WPI; 93-272883/34.
                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus. W09316179-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Son of sevenless gene; m
tyrosine kinase; tumour.
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26-MAY-1994
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                                                                                                                                           N-PSDB; Q48610
                                                                                                                                                                                                                                                                                          17-FEB-1992; AU-000921
                                                                                                                                                                                                                                                                                                             19-AUG-1993.
17-FEB-1993; AU0068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalian
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58; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 (first entry) son of sevenless
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364 AA;
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larity 25.48;
Conservative
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gene; mSos; Sos; guanine exchang
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Pred. No. 3.02e-10;
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R84638 stand
R84638;
25-FEB-1996
                                                          Detection of agents that modify BCR-ABL mediated transformation useful in treatment of leukaemia and other malignancies Disclosure; Page 54-59; 106pp; English.

Mouse mSOS1 (R84638) is a Ras guanine nucleotide releasing protein that combines with BCR-ABL and Grb2 (R84636) to activate the Ras pathway leading to morphological transformation. The SH3 domains of Grb2 associate the the proline-rich domains of mSOS1 and mSOS2 (R84639). Synthetic peptides (R84640-48) based on these motifs can be used to screen for compounds that affect BCL-ABL mediated transformation. Such compounds have value in the treatment of chronic, acute myelogenous or acute lymphocytic leukaemia. Sequence 1336 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Figure 1; 78pp; English.

The mammalian son of sevenless gene has been found to have homology with various quanine exchange factors, suggesting a possible role in protein tyrosine kinase pathways via the Ras proteins. Mutations in the genes and consequently their products may result in specific defects or tumour formation. Antagonists to the protein/gene may be used to treat conditions arising from mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mSOS1 protein.
mSOS1; SOS1; Grb2; BCR-ABL; oncoprotein; leukaemia; Ras
                                                                                                                                                                                                                                                                Arlinghaus R, Gisl
WPI; 95-302931/40.
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14-JAN-1994; CA-113494.
(MOUN ) MOUNT SINAL HOSPITAL CORP.
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58; Conser
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64; Mismatches 98
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05-SEP-1997; G02394.
08-APR-1997; GB-007132.
06-SEP-1996; GB-018600.
(CLIN-) CENT CLINICAL & BASIC RE
BYTJALSEN I, Fey SJ, Larsen P;
WPI; 98-207057/18.
Homo sapiens.

W09853061-A1.

26-NOV-1998.

22-MAY-1998; AU0380.

22-JAN-1998; AU-001460.

23-MAY-1997; AU-006972.
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An alternati
MCG4 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 12
W87995
W87995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochemical markers of human endometrium - useful for, e.g. diagnosis of hyperplasia and adenocarcinoma Disclosure; Page 19-20; 77pp; English. Proteins w54349-W54364 are examples of proteins produced in the endometrium during the hyperplasia, adenocarcinoma or proliferative phase of the endometrium. The presence and quantities of these proteins can be detected using 2D gel electrophoresis comparison of cell lysates. The proteins can be used as biochemical markers to detect the phase of the endometrium and can be measured in body fluids, obviating the need for endometrial biopsies.
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Similarity 31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 AA;
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                                                                                                                                                                                                                                                         pliced human MCG7 protein.
regulatory function; heat shock protein;
exchange factor protein; MCG7 protein;
protein; MCG18 protein; zinc finger prote
                                                                                                                                                                                                                                                                                                                                                                                                              entry)
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Pred.
26; M
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No. 5.94e-06
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                                                                                                                                                                                                                                                                 7 protein;
finger protein;
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Best Local 9
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                                                                                                                                                                                                                                                                                                Homo sapiens.
W0985361-A1.
26-NOV-1998.
22-MAY-1998; AU-001460.
22-JAN-1998; AU-006972.
23-MAY-1997; AU-006973.
23-MAY-1997; AU-006974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New gene-expression regulatory genes, mcg4, mcg7, and mcg18 - encode a zinc finger protein, a GEF, and a heat shock or heat shock binding protein, useful to detect and treat cancer claim 5; Fig 13b; 80pp; English.

The present sequence represents a MCG7 protein. The protein has gene regulatory functions, and has homology to a heat shock protein or heat shock-binding protein. The specification also describes MCG4, which is homologous to guanine nucleotide exchange factor protein, and MCG18, which is homologous to a zinc finger protein.

Detection of mutations in the MCG genes can be used to identify the propensity for various types of cancer, and to treat, arrest, or otherwise ameliorate, the effects of a cancer in an animal or bird.
New gene-expression regulatory genes, mcg4, mcg7, and mcg18 - encode a zinc finger protein, a GEF, and a heat shock or heat shock binding protein, useful to detect and treat cancer claim 5; Fig 13a; 80pp; English.

The present sequence represents a MCG7 protein. The protein has gene regulatory functions, and has homology to a heat shock protein or heat shock-binding protein. The specification also describes MCG4, which is homologous to guanine nucleotide exchange factor protein, and MCG18, which is homologous to a zinc finger protein.

Detection of mutations in the MCG genes can be used to identify the propensity for various types of cancer, and to treat, arrest, or
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23-MAY-1997; AU-006974.
22-JAN-1998; AU-001458.
22-JAN-1998; AU-001459.
(COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
Gartside M., Grimmond S, Hancock J, Hayward N
                                                                                                                                                                                                                      23-MAY 199; AU 001458.
22-JAN-1998; AU-001459.
22-JAN-1998; AU-001459.
(COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCG4 protein; gene regulatory function; heat shock protein; guanine nucleotide exchange factor protein; MCG7 protein; heat shock-binding protein; MCG18 protein; zinc finger protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W87994;
15-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W87994 standard;
                                                                                                                                                                                              WPI; 99-070146,
N-PSDB; X04552.
                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A human MCG7 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PETIKLWEGLTELVTATGNYGNYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLMI-LSKPTAPQRALVITHFVHVAEKLLQLQNFNTLMAVVGGLSHSSISRLKETHSHVS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FDHLEPMELAEHLTYLEYRSF-C-KILFQDYHSFVTHGCTVDNPVLERFISLFNSVSQWV 207
                                                                                                                                                                                                               99-070146/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTEICLCSQLS-KRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSRLALTWEKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.98;
Similarity 26.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        609 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
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Pred. No. 2.
34; Mismatc
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.29e-04;
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t shock binding
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                                                                                                                                                                                                                                                                per Determining effect on signalling pathways in live cells from redistribution of luminophores - specifically fusions of green fluorescent protein with a signalling component, and new apparatus, per particularly for identifying toxins and potential therapeutic agents Example 10; Pages 281-283; 326pp; English.

The present sequence represents a human PKG-green fluorescent protein (GFP) fusion protein. The fusion protein is used in an assay to exemplify the invention. The specification describes how quantitative information about the influence of a molecule on a cellular response is obtained by recording the variation, caused by the molecule on mechanically intact living cells, in the spatially distributed light emitted from a luminophore present in the cells. The variation in light distribution to the degree of the molecule. The method is used to identify agents that (in)directly affect intracellular signalling, especially to screen for potential therapeutic agents or toxins, and to identify new drug targets.
                                                                                                                                                                                      Query Match
Best Local S
Matches 3
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07-APR-1998; DK0145.
07-APR-1997; DK-000392.
(NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intracellular signalling;
Chimeric - Aequorea victo
Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; V71085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kasper A, Petersen
Tullin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W85040;
08-FEB-1999 (first entry)
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                                                                                            286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 666 VTEICLCSQLS-KRVQLLKKFIKIAAHCKEYKNLNSFFAIVMGLSNIAVSRLALTWEKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 FDHLEPMELAEHLTYLEYRSF-C-KILFQDYHSFVTHGCTVDNPVLERFISLFNSVSQWV
299 E 299
                             344 D 344
                                                                                                                         186 YEELLH-IKALSHLSTTVKRELAGVLIFESHAKGGTVLFNQGEEGTSWYIILKGSVNVVI 244
                                                                                                                                             YMEFLKSVPTFQSLPEEILSKLADVLE-ETHYENGEYIIRQGARGDTFFIISKGTVNVTR 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98-594491/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLMI-LSKPTAPQRALVITHFVHVAEKLLQLQNFNTLMAVVGGLSHSSISRLKETHSHVS 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKFKKFYAEFESLMDPSRNHRAYR 748
                                                               --Y-GKG-V-VCTLHEGDDFGKLALVNDAPRAASIVLRED-NCHFLRVDKEDFNRILRDV
                                                                                            EDSPSEDPVFLRTLGKGDWFGEKALQGEDVRTANVIAAEAVTC--LVIDRDSFKHLIGGL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.98;
Similarity 26.48;
38; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKG gene; fusion protein;
                                                                                                                                                                                     h 2.2%;
Similarity 30.6%;
37; Conservative
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                                                                                                                                                                                                                                                       932 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aequorea victoria.
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                                                                                                                                                                                      Score 134; DB 1; 1
Pred. No. 4.81e-01;
28; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scudder K, Thastrup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 180; DB 1;
Pred. No. 2.29e-04;
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PT redistribution of luminophores - specifically fusions of green redistribution of luminophores - specifically fusions of green fluorescent protein with a signalling component, and new apparatus, per particularly for identifying toxins and potential therapeutic agents per particularly for identifying toxins and potential therapeutic agents for protein 10; Pages 274-276; 326pp; English.

CC PKG fusion protein. The fusion protein is used in an assay to complify the invention. The specification describes how quantitative information about the influence of a molecule on a cellular response is contained by recording the variation, caused by the molecule, on mechanically intact living cells, in the spatially distributed light emitted from a luminophore present in the spatially distributed light cemission is processed to provide information that correlates spatial constitution to the degree of the molecule. The method is used to identify agents that (in)directly affect intracellular signalling, contained to the specially to screen for potential therapeutic agents or toxins, and to
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Best Local :
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07-APR-1998; DK0145.
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(NOVO ) NOVO-NORDISK AS.
Kasper A, Petersen Bjorn S, S
Tullin S;
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Chimeric - Aequorea victoria.
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Human; PKG gene; fusion protein; green fluorescent protein; GFP;
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W85039;
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299 E
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28; Mismatches 46
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